


```

QY 479 LeuLysHisIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGlu 498
Db 262 -----AAAGGTGATCAAAATCGAAATCGCAATTTGAT 297
QY 499 TyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPhe 518
Db 298 TTTTCAGAACTTCT-----TTTCAGAAACCCAGCTGTTTATTATTATAC 339
QY 519 ThrAspSerIleGlu-----LeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAsp 537
Db 340 AAAGTAACTGAGAGAGATGATTAAGTTCCTGGCTTCTTAT----- 384
QY 538 MetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsn 557
Db 385 -----GATACAACTGCTTCACTGTTCAAGTTCATCTCTTGAGATGAAGACACAA 438
QY 558 ProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnLysTyrGlnSerLeu 577
Db 439 AAACCGATAGCTACT-----TATATT 459
QY 578 IleGlyThrGlnThrPheProGluAspLeuValAspIleIleArgMetGluAspLysLys 597
Db 460 GTTGGTTATATA-----GAAGGTAGTAG 483
QY 598 GluValIleProVal-----ThrHisAsnLeuThrLeuArgLys 610
Db 484 -----GTGCCAATTCAGTTCAAAAATAGCTTAGATTCTACTCATTAACGGTGAAGAAA 537
QY 611 ThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLys 630
Db 538 AAAGTTCAGGTCCGGTGGAGATCCCTTAAGATTTTATTTTGGTTCAGCTTTTAAAA 597
QY 631 AsnAspLysGlnLeuLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe 650
Db 598 GCAAATCAGATATATTAAGGGGTCAAGAAAAGTCATGATTAAGAGACAACT----- 648
QY 651 LysAspGlyLysAlaThrIle-----Asn 658
Db 649 AAAGGTGTCACACTCTCTTCAACAGAGCTAGTATAGATCAACTCATATTATTTACC 708
QY 659 LeuLysHisGlyLysLeuSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuVal 678
Db 709 TTGAAGATGGTAAATCAATCAAAAGTCACAAATCTTCAGTAGCTGATTTATGTTGTC 768
QY 679 LysGluThrAsp-----SerGluGlyTyr-----LysValLysValAsnSerGlnGlu 694
Db 769 ACTGAGAGAGCATTAACAATCAGAAAATATACAAACCAAGCTGGAAGTACTCTCAAGAT 828
QY 695 ValAla-----AsnAlaThrValSerLysThrGlyIleThrSerAsp 708
Db 829 GGAGCTGTAAAAAATATCGCAGGTAAATTCAACTGACACAGACAGCACTACTGATAAAGAT 888
QY 709 GluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAspGlnLys 728
Db 889 ATGACCATTAATCTTCAAAATTAATAAAGATTGGAAGTCCAAACAGAGTAGCAATGACT 948
QY 729 IleAsnGlyTyrLeuAlaLeuIleValIleAla 739
Db 949 GTGGCACATATATTCCTTAGCAATTTGATGA 981

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XX OS Enterococcus faecalis.
XX PN WO9850555-A2.
XX PD 12-NOV-1998.
XX PF 04-MAY-1998; 98MO-US08985.
XX PR 14-NOV-1997; 97US-0066009.
XX PR 06-MAY-1997; 97US-0044031.
XX PR 16-MAY-1997; 97US-0046655.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Barash SC, Dillon PJ, Kunsch CA;
XX DR WPI; 1999-045171/04.
XX PT New isolated Enterococcus faecalis polynucleotides and polypeptides
XX PT - used to develop products for the detection of Enterococcus and for
XX PT use in vaccines for prevention or attenuation of Enterococcus
XX PT infection.
XX PS Claim 1; Page 419-427; 2084pp; English.
XX CC A computer readable medium has been developed which has recorded on it
XX CC 992 nucleotide sequences isolated from the Enterococcus faecalis genome.
XX CC AAX12982 to AAX13919 represent these nucleotide sequences which are
XX CC primary nucleotide sequences, also known as contigs. The computer-based
XX CC system can identify fragments of the Enterococcus faecalis genome with
XX CC commercial importance. The products can be used to detect the presence
XX CC of Enterococcus faecalis in samples. They can also be used for
XX CC diagnosing Enterococcal infection in an animal and monitoring
XX CC progression of disease, and for identifying agents which can be used to
XX CC modulate the growth or pathogenicity of Enterococcus faecalis, or
XX CC another related organism, in vivo or in vitro. In particular the
XX CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
XX CC can be used in vaccines to prevent or attenuate an Enterococcal
XX CC infection.
XX SQ Sequence 15614 BP; 5535 A; 2567 C; 3169 G; 4326 T; 17 other:

Alignment Scores:
Pred. No.: 8.13e-05 Length: 15614
Score: 196.00 Matches: 165
Percent Similarity: 35.57% Conservative: 89
Best Local Similarity: 23.11% Mismatches: 245
Query Match: 4.97% Indels: 216
DB: Gaps: 41

US-09-494-297-2 (1-757) x AAX12982 (1-15614)
QY 88 PheArgValAlaHisAspLeuArgValAsnLeuGlySer-----ArgSerTyrGln 105
Db 9047 TTCAAGTTCAAACATTA-CCGAAGTGTCTCAACAGCCCTCAATTAATATATGAG 9105
QY 106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLys 125
Db 9106 ATTTAT-----TTGGGTAAAGGCAAGAAATTCAAAT 9138
QY 126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp----- 139
Db 9139 CATTATCAACTAGCT-----ATTCAACAGAGTCAAGAAAACCTCAACCTGATTTTGG 9192
QY 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
Db 9193 TATCAATATGATGTGGACACAGTTTCAGCCATTCAGCCAGCCGCCCTGAAAAAGTTGAT 9252
QY 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179
Db 9253 TTT-----GGGTTCTTCCTGGGAAAAAGCACCT-----GGC 9282

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RESULT 3
AAX12982
ID AAX12982 standard; DNA; 15614 BP.
XX
AC AAX12982;
XX
DT 19-MAR-1999 (first entry)
XX
DE Enterococcus faecalis genome contig SEQ ID NO:45.
XX
KW Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.

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OY	180	lleargValthrGlnGlnLualavaLTPpTYrTYrSerSaspashAlaProIlesSeraspPro	199
Db	9283	GTGAAGTTAAACGTGAAAAAAATCTCGGAAGAGTATGATCAAGACCCGACAATCGGCCA	9342
OY	200	AspGluSerhellysArngLuserSerAsnLueValSerThSer-----	215
Db	9343	GATAAATGCTATTATATGAAATTAAGTACAAAGCAAGTAAGTACACACACCACCAATGGCAAACT	9402
OY	216	-----GlnLeuSerLeuMetArgLlnAlaLeuLysGlnLeuLileasProAsnLeu	232
Db	9403	GGGATATTATTAATTATCAAAACCAAGAAAATGATACACGCAATATGTTGGAGGCGCAAAAT	9462
OY	233	AlaThrLysMetProLysGlnValProaspPheGln-----LeuSerLlePheGlu	250
Db	9463	GTAAACCCAACTTCCAAAACCCGGGATGAAGACTATCAAGAAAGTCTTCGGCTCCCA	9522
OY	251	SeerLusPlysgLysPlystyAsnLysGlyTYrGlnAsnLeuLeuSerLylGlyLeu	270
Db	9523	TACACAAATCAAGACACAGCTTCAAT-----TATCAAAACAACCCGTAATTACA--	9573
OY	271	ValProThrLysProProThrProGlyAspProPomeProPomeProAsnGlnProGlnThr	290
Db	9574	GTTCCTCGTTACAGTCAAGAAAAAATCGACGATACACTGTGAAAAACACGAAGCATTC	9633
OY	291	ThSerVal-----LeuLleArgLysTYrAlaLleGlyAspTYrSerLysLeuLeu	307
Db	9634	AAGCATTACATTTTAAAGTAACCAAAAATTCCTCCAGGTGAG-----AAAAACTTA	9687
OY	308	GluGlyAlaThrLeuGlnLeuThrGngLysAspAsnValAsnSerPheGlnAlaArgAlaPhe	327
Db	9688	GTGGAGACCGCTCTTGATTAATGATGGTGAATAAATGTT-----CAAAACAATTAAGTG	9738
OY	328	SeSerAsnasp-----LleGlyLArgLleGluLeuSeraspLys--Thr	342
Db	9739	GACATTAAGAATGGTAGCTATTCCTCCCAAAAAGATGTCGCCCTACAAAABAGGAGACCG	9798
OY	343	TYrThrLeuThrGluLeuAsnSerProAlaGlyTYrSerLleAlaGluProIleThrPhe	362
Db	9799	TATTCATTAACTGAAGTAAGTAAGCACTCGGACGACATGATTAAGCAAGAAAACGACTGG	9858
OY	363	LysValGlnLue-----GlyLysValTYrThrLleLleAspLysLysLlnLleGlu	379
Db	9859	CAAAATTAGCTAGTGAAGCAAGCAAAAGTA-----AGCATGATGAGCAACAAAGAGACC	9912
OY	380	AsnProAsnLysGlnLleValGluProTYrSerValGlnAlaTYrAsnaspPheGluGlu	399
Db	9913	ACCACAATCAATCACTATT-----CCATTGGAAATTGAA-----AATAAATTTCTTCT	9960
OY	400	PheSerVal-----LeuThrThrGlnAsnTYrAlaLysPheTYrTYrAlaLys	415
Db	9961	TTGGCAATTCAGAAATTAGAAAATATACACCATGCAAAAT-----GGCAAA	10002
OY	416	AsnLysAsnLysSerGlnValValTYrCysPheAsnAlaAspLysLysSerProBr	435
Db	10003	CAAGTGAACCTTACACAGCGGACCTTTGGCTTCCAAAAGA-----	10042
OY	435	oAspSerGluAspGlyLysThrMetThrProaspPheThrGlyGluValLysTY	455
Db	10043	-----AAAATGCTGCACGAAGACTTACCAAACTGTGGCAACTCAAAA	10083
OY	455	rThrHisLleAlaGlyArgAspLeuPheLysTYrThrValLysProArgAspThrAspPr	475
Db	10084	AACGATACATACAGAGATAGACATATT-----	10111
OY	475	oAspThrPheLeuLysHisLleLysLysValleGluLysGly--TYrArgLuuLysG	494
Db	10112	-----AAAATTAAGTGAACCTGTGAGTATCGA-----	10138
OY	494	YglnAlaLleGluTYrSerGlyLeuThrGlnLeuArgAlaAlaLleThrGlnLueAl	514
Db	10139	-----ATGGTGAACAATCAAGA-----CCATTAGGCTACGACACCTTGGCTGG	10182
OY	514	aLleTYrTYrPheThrAspSerAlaGluLeuAspLysAspLysLueLysAspTYrHisG	534


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Oy 554 n-----AspSerAsnProGlnLeuThraspleuAspPheIleProAsnAs 571
Db 10231 CAAAAATATGAGAAATGCGCCAGATGAGACA----- 10264
Oy 571 nasulysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleI 591
Db 10264 ----- 10264
Oy 591 eaRgMeCluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLys-- 610
Db 10265 -----CTGACACATCAAAATAATTAATTTGAAACCTTT 10293
Oy 611 -----ThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleG 628
Db 10294 TGACTTAACAGTATTAATAAAAGCCGATATACAGC-----CC 10332
Oy 628 uLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLe 648
Db 10333 ACTTAAGAGCAGAAATTCGTTTAACAGCA-----CCAGATACGATAT 10377
Oy 648 uGluPhe---LysAspGlyLysAlaThr-----IleAsnLeuLysHisG 662
Db 10378 TGAATTAACAAAGATGCAAGAAACGATCTTTGTTTGAATACTTAATAAACCCAG 10437
Oy 662 YGU---SerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGluTh 681
Db 10438 GAAATATGTTTAAACAGAACCTTTACGCCAGAGGATATACAGGGGTTTAAAGAACCAAT 10497
Oy 681 rAsp-----SerGlnGlyTyrLysValLysValLysAsnSerGlnGluValAlaAsnAl 698
Db 10498 CGAATTATATATGCTGAGAAAGTTCAGTCACGATAGATGGGAAAGTAGCAGATGT 10557
Oy 698 aThrValSer-----LysThrGlyIleThrSerAspGluThrLeuAlaPheGluAs 715
Db 10558 TTTAATTTCTGAGAGAGAAATCAAAATTAATTAATTAATTAATTAATTAATTAATTA 10608
Oy 715 nasuLysGluProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLe 735
Db 10609 AGCAAAAGTCTCTTACCTGAACACTGTGCGATAGAGAGCGTTGGTGTCTTACTGATAGC 10668
Oy 735 uIle-----ValIleAlaGlyIleSerLeuGlyIle 745
Db 10669 GATTAGTACATTCGTCGATAGCGGCTTATCTCTTTATT 10708

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RESULT 5
AAA30874
ID AAA30874 standard; DNA: 2127 BP.
XX AAA30874;
AC
XX
XX 19-SEP-2000 (first entry)
DT
DE Streptococcus equi fibronectin binding protein, FNZ, coding sequence.
XX
XX Fibronectin binding protein: SFS; vaccine; horse; strangles; therapy;
KW equine upper respiratory tract disease; S. equi infection; FNZ; ds.
XX
OS Streptococcus equi.
XX
XX Key location/Qualifiers
XX CDS 108..1901
XX FT /*tag=a
XX FT /product= FNZ
XX
XX MO2000037496-A1.
XX
XX 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-S020448.
XX
XX 22-DEC-1998; 98SE-0004491.
XX
XX (GUS5/) GUS5 B.

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PA (LIND/) LINDMARK H.
PA (JACO/) JACOBSSON K.
PA (FRK/) FRKBERG L.
XX
XX Guss B, Lindmark H, Jacobsson K, Frykberg L;
DR WPI: 2000-442641/38.
DR P-PSDB: AAV90257.
XX
XX New protein useful for preparation of vaccines for treatment of
XX strangles caused by Streptococcus equi infection, is able to bind to
XX mammalian fibronectin -
XX
XX PS Disclosure: Page 17a-17d; 34pp; English.
XX
XX This sequence encodes the Streptococcus equi fibronectin binding
XX protein FNZ. The FNZ sequence was used to isolate the S. equi fibronectin
XX binding protein of the invention, designated SFS. SFS binds specifically
XX to mammalian fibronectin or its analogues or fragments. The protein, its
XX analogues or fragments may be used for the preparation of a vaccine that
XX protects horses against strangles (a world-wide distributed and serious
XX disease of the equine upper respiratory tract) caused by S. equi
XX infection. The antibody and/or antiserum may also be used for the
XX prophylactic or therapeutic treatment of S. equi infection in mammal,
XX especially horses. The use of vaccines containing the fibronectin binding
XX protein provides a more effective protection against S. equi infections,
XX with fewer side effects.
XX
XX SQ Sequence 2127 BP; 718 A; 415 C; 466 G; 528 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0.000124 Length: 2127
XX Score: 180.00 Matches: 150
XX Percent Similarity: 34.64% Conservative: 98
XX Best Local Similarity: 20.95% Mismatches: 270
XX Query Match: 4.56% Indels: 198
XX DB: 21 Gaps: 33
XX
XX US-09-494-297-2 (1-757) x AAA30874 (1-2127)
Oy 68 serGluTyrArgTyrGlyTyrGlyLysSerTyrValArg---GlyHisProTyrTyrLys 86
Db 201 GCAGAGCAGCTTATATATGCGTGAATGATGAGACAGCAAAAGTCCCATATTTT--- 257
Oy 87 GlnPheArgValAlaHisAspLeuArgValAsnLeuGlnGlySerArgSerTyrGlnVal 106
Db 258 ---TTGTACGATATCCCTAAATAATGCTCAAAAGCTGCAATTTAAAGACGATATGTT 314
Oy 107 TyrGlyPheAsnLeuLysLysAlaPheProLeuGlySerAspSerValLysLysTyr 126
Db 315 TATTGCTTTAAACAAATAATGTATATGCGCAGATCAATGGGAATCTATATACAGCAATTTT 374
Oy 127 -----TyrLysLysHisAspLysIleSer 134
Db 375 AATGACATCAGATTCATATATACGATTTACCTGATATATGAGAAAAAAGTACGATATCAT 434
Oy 135 ThrLysPheGluAspTyrAlaLeuSerProArgIleThrGlyAspGluLeuAsnGlnLys 154
Db 435 GGTATATTTAAACAATATGCTCCAGATTAACAATAAAGATATATAGATATTCACAGTCT 494
Oy 155 LeuArgAlaValMetTyrAsnGlnLysProGlnAsnAlaAsnGlyIleMetGluGly--- 173
Db 495 TTGGTGCGAGTTTAAATGATGATATGCAATCCCACTAAAGTCAACATCACTACAGTAC 554
Oy 174 ---LeuGlnProLeuAsnAlaIleArgValThrGlnGluAlaValTyrTyrTyrSerAsp 192
Db 555 CATTTAATATATGATCTTCTAGAAAAGTATCTACATATGATATTTGATATTTGATAT 614
Oy 193 AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGluSerAsnLeuVal 212
Db 615 -----AGTTTAACAAGAAAGATACCTTAAGATACGGGCTTATTAACCTTA--- 659
Oy 213 SerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232

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Db 660 -----AACGATATGAGAAAAAAGCTTTAGATTATTAACAGTAAAGAGAG 707
QY 233 AlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGlnSerGlu 252
Db 708 GATCTTAGCTT---AAATCAGAGCAGAGTAAATACCATGGATATTATTTATGTTTATCA 764
QY 253 AspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValPro 272
Db 765 AGTGGGGGGCATGACCATGATAAAGATTACCAAAATCTCTCGGCTTACTTAAATTCCT 824
QY 273 ThrLysProProThrProGlyAspProIometProProAsnGlnProGlnThrSer 292
Db 825 AAAGAACCCGCTAAAGCTT----- 842
QY 293 ValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGlnGlyAlaThrLeu 312
Db 843 -----CAGCTAGGCTTTAGT----- 860
QY 313 GlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIle 332
Db 861 -----GGACATATATGAAATGATTAAGCGCCTTGAAGAGAGATCATCATGTTCA 911
QY 333 GlyGlnArgIleLeuLeuSerAspGlyThrTyrThrLeuThrGlnLeuAsnSerProAla 352
Db 912 CAAGAAACTAATGAA-----GATGTTAAGAAAGACTT-----ATAGTTTCCATGGA 959
QY 353 GlyTyrSerIleAlaGlu-----ProIleThr---PheLysValGlnAlaGly 367
Db 960 GGCATCTCAGAAAGCCAGCCAAACAGATCTTTGGCAGAGATTGAAGGGTGAAGCTGGT 1019
QY 368 LysValTyrThrIleLeuAspGlyLysGlnIleGlnAsnProAsnLysGlnIleValGln 387
Db 1020 GCACATGATACA-----CTCAAAAGCCTAATGATCATGTCATG----- 1055
QY 388 ProTyrSerValGlnAlaTyrAsnAspPheGlnGluPheSerValLeuThrThrGlnAsn 407
Db 1056 ---CAAGCTTTAAGCGGTAAAC-----CTCCTAATAGTAAAGCAAAAC 1097
QY 408 TyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPhe 427
Db 1098 TATGTAGT-----ACCGAAGCATATGATGTCATCATCAGGCATTTCTGAG----- 1142
QY 428 AsnAlaAspLeuLysSerProAspSerSerGluAspGlyLysThrMetThrProAsp 447
Db 1143 GAAGACGAGATACCTAACCCACTGATCATGATCGGCGGCTAGCTGAGC 1199
QY 448 PheThrThrGlyGlnValLysTyrThrHisIleAlaGly-----Arg 461
Db 1200 ---ACCGATGAAATACTATCAAAACCCATCATGATGGGATCGCGGCTAGCTGAGC 1256
QY 462 AspLeuPheLysTyrThrValLysProArg-----Asp 472
Db 1257 GAATCAAGAGAAACGACCTAAACGACAAACCGCGCGGCAAGAGCAGCATGCTAGC 1316
QY 473 ThrAspProAspThrPheLeuLysHisIleLysValIleGlnLysGlyTyrArgGln 492
Db 1317 ACACAGAGAGATACA-----CAA 1334
QY 493 LysGlyGlnAlaIleLeuTyrSerGlyLeuThrGlnThrGlnLeuArgAlaIleThrGln 512
Db 1335 AAAGGATGCTCTGACATCTGCTGCTACTATGAGTCAAGAAACACCAAAAGCCGAG 1394
QY 513 LeuAlaIleLysTyrThrThrAspSerAlaGlnLeuAspLysAspLysAspTyr 532
Db 1395 GTATGATTGTGGTCTAGAGCAAAACCATCGACAGACAAACACACACACAAAAA----- 1448
QY 533 HisGlyPheGlyAspPheLysAsnSerThrLeuAlaValAlaLysIleLeuValGlnTyr 552
Db 1449 ---GGCATGCTCTGACATCTGCGGCTACTATGAG----- 1481
QY 553 AlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsn 572
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Db 1482 TCAGAGCAGACTAAGAAACCTGAGTC----- 1508
QY 573 LysTyrClnSerLeuIleGlyThrGlnThrHisProGlnAspLeuValAspIleIleArg 592
Db 1509 -----ATGATGGTGGTCAG----- 1523
QY 593 MetGlnAspLysLysGlnValIleProValThrHisAsnLeuThrLeuArgLysThrVal 612
Db 1524 -----GGACAAATCATCGACTCTCTGAGAGATACAGCCGGGTATGCTGGT---CAATCT 1688
QY 613 ThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGlnIleGlnLeuLysAsnAsn 632
Db 1566 TCTGGCGAGCTGCTGTCAGCTAGC-----GTAATTGAG----- 1598
QY 633 LysGlnGlnLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGlnLysPheLysAsp 652
Db 1599 -----GATACCAAGAGCTGAGATATCATATTGGTGGG 1631
QY 653 GlyLysAlaThrIleAsnLeuLysHisGlyGlnSerLeuThrLeuGlnGlyLeuProGln 672
Db 1632 CAAGGACAAATCATCGACTCTCTGAGAGATACAGCCGGGTATGCTGGT---CAATCT 1688
QY 673 GlyTyrSerTyrLeuValLysGlnThrAspSerGlnGlyTyrLysValLysValAsnSer 692
Db 1689 GGAGGCACTCAATTTGCGAAGACACCAAGACCCGACACTAAGCCTTAACCTGCACCT 1748
QY 693 GlnGlnValAlaAsnAlaThrValSerLysThrGlyLleThrSerAspGlnThrLeuAla 712
Db 1749 GCGCCAAATTTTAAT-----GACGAA----- 1769
QY 713 PheGlnAsnAsnLysGlnProValIleProThrGlyValAspGlnLys----- 728
Db 1770 ---AAACCTAACAAGGCACTCATCTCCACAGACAAAGTATGAAGCAACACCTCA 1826
QY 729 ---IleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyLysLeuLeu 743
Db 1827 AGCATCATCGTGCATGCAATGCAATGCTGCTGCTATGCTGCTCA 1874

RESULT 6
AAV82019
ID AAV82019 standard; DNA: 7650 BP.
AC AAV82019;
XX 21-JUN-1999 (first entry)
DE Moraxella catarrhalis 4223 lfr region.
XX
KW Lactoferrin receptor; lactoferrin binding protein; LBPI; LBPI2;
KW lbpA gene; lbpB gene; ORE3; infection; otitis media; sinusitis;
KW conjunctivitis; pneumonia; bronchitis; tracheitis; emphysema;
KW diagnosis; therapy; vaccine; Branhamella catarrhalis; ss.
XX
OS Moraxella catarrhalis.
XX
FH Key Location/Qualifiers
FT -35_signal 64..69 /*tag= a
FT -10_signal 98..103 /*tag= b
FT RBS 127..136 /*tag= c
FT CDS 141..2837 /*tag= d
FT /gene= lbpB
FT /product= LBPI2
FT /transl_except= (pos:2031..2032, aa:Asn)
FT /note= "this codon has an apparent 1 codon deletion
FT which alters the reading frame"
FT /transl_except= (pos:2036..2039, aa:Ala)
FT /note= "this codon has an apparent 1 codon
FT insertion which alters the reading frame"
FT /note= "lbpB is specifically claimed in Claim 8;

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FT misc_feature 632 encodes AAM89413"

FT /tag= e

FT /note= "this base is not present in the sequence

FT given in the specification, the nucleotide

FT has been included to maintain the reading

FT frame as part of a codon (AAR) for Lys"

FT -35_signal 2973..2978

FT /tag= f

FT 2990..2995

FT /tag= g

FT 3006..3015

FT /tag= h

FT 3021..6023

FT /tag= i

FT /gene= lbpa

FT /product= LBp1

FT /note= "specifically claimed in Claim 8; encodes

FT AAM89414"

FT CDS 3066..6023

FT /tag= j

FT /gene= lbpa

FT /product= LBp1

FT /note= "specifically claimed in claim 8; encodes

FT AAM89415"

FT 6025..7650

FT /tag= k

FT /gene= orf3

FT /note= "specifically claimed in Claim 7; encodes

FT AAM89416"

FT W09855606-A2.

PD 10-DEC-1998.

XX 02-JUN-1998; 98WO-CA00544.

XX 08-MAY-1998; 98US-0074658.

PR 03-JUN-1997; 97US-0867941.

XX (CONN-) CONNAUGHT LAB LTD.

PA Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;

PI WPI: 1999-070266/06.

DR P-PSDB; AAM89413, AAM89414, AAM89415, AAM89416.

XX Lactoferrin receptor genes from Moraxella, especially M. catarrhalis

PT - useful to diagnose Moraxella infection e.g. to detect otitis media

PT due to M. catarrhalis infection and to immunise against such

PT infections

XX Claim 8; Fig 2A-2P; 202pp; English.

PS This polynucleotide comprises the lactoferrin receptor (lfr) locus

XX of Moraxella catarrhalis (Branhamella catarrhalis) 4223. There are

CC 3 tandem genes in locus, identified as lbpa, lbpb (alternative

CC start codons) and orf3a, respectively encoding lactoferrin binding

CC protein 2 (lbpb2, see AAM89413), lactoferrin binding protein 1 (lbpl,

CC see AAM89414 and AAM89415) and open reading frame protein 3 (orf3, see

CC AAM89416). The lfr locus was identified following generation of a M.

CC catarrhalis strain 4223 genomic DNA library and screening with a

CC specific hybridisation probes. The genes and DNA sequences of the

CC lfr locus are useful for diagnosis, immunisation, and the

CC generation of diagnostic and immunological reagents. Immunogenic

CC compositions, including vaccines, based upon expressed recombinant

CC lbpl and/or lbpb2 and/or orf3, portions of these or their analogues,

CC can be prepared for prevention of diseases caused by Moraxella. M.

CC catarrhalis is a causative agent of otitis media and has been

CC associated with sinusitis, conjunctivitis and inflammatory diseases

CC of the lower respiratory tract, such as pneumonia, chronic

CC bronchitis, tracheitis and emphysema.

SO Sequence 7650 BP: 2410 A; 1741 C; 1636 G; 1862 T; 1 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
Score:	178.00	171	118	305	42
Percent Similarity:	31.48%				
Best Local Similarity:	18.63%				
Query Match:	4.51%				
DB:	20				

US-09-494-297-2 (1-757) x AAV82019 (1-7650)

QY 4 ThrArgPheProAsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSer 23

DB 375 ACAACTGACCCAAATGGCGATACACCAACTGACACAA----- 413

QY 24 LysArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43

DB 414 GCACAAAGACCGCGCGCTGCCAGGCTTTTGTGATG----- 452

QY 44 MetValGlyAlaLysThrValPheGlyLeuValGlySerSerThrProAsnAlaLeuAsn 63

DB 453 -----GTTAAATTTCGTGATACCAAGCCCAAAAT--GAC 485

QY 64 ProAspSerSerGluLys-----TyrArgTyrPyrGly-----TyrGlySerThrVal 79

DB 486 CCAGATTATAGCAATGATTTAGTACGAGTGGCAAGCAATATATATGTTGGTATTCAT 545

QY 80 ArgGlyLysPro----- 83

DB 546 GCCCATCGCCCGATGCGCATCGGCACAGTAAACCTTCGTCACCCCATCCGCCCAAT 605

QY 84 -----TyrTyrLysGlnPheArgValAlaAlaHisAspLeuArgValAsnLeu 98

DB 606 GACATCAAAACCTTGTATTTTACCAARCTCCCTGATGTGTGATTCGATTTAGACAGT 665

QY 99 GluGlySerArgSerTyrGlnValTyrTyrPheAsnLeuLysLysAlaPheProLeuGly 118

DB 666 GAACGCCACCGT--TTTGACCCCAAAAGCTAAACACCATTAAGTATGTTATGTCG 722

QY 119 SerAspSerSerValLysLys-----TrpTyrLysHisAspGlyIleSerThrLys 136

DB 723 AACTTAACACACCCCTGTAATAAACACACTTCATCATCATCAGACAGCTATATAAG 782

QY 137 PheGluAspTyrAlaMetSerPro-----ArgIleThr 147

DB 783 AAAAATTAACAGCCCTGTGACCTTATGATAAATATCCGTTGGTATCTTGACTACAA 842

QY 148 GlyAspGluLeuAsnGlnLys----- 154

DB 843 GGAAGCAGCTGTGACCCCAAAATGCCGATCTCCAAATGACAAAGACCGCATTCACAA 902

QY 155 --LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly 173

DB 903 CCCATGCCCATTTTGTTTTATATCAGCA-----GAAACGCCAGCAGCAGTCCCACT 956

QY 174 LeuGluProLeuAsn----- 178

DB 957 GCTGTAAATTAATTAACTACACAGCACTGCTGTACTAAGTATGATCAAAAAAGCCCT 1016

QY 179 AlaIleArgValThrGlnGluAlaValIrrPyrTyrSerAspAsnAlaProIleSerAsn 198

DB 1017 GCACCTTCAGCATCAGATGATGAGTGGGCTCTATTCATCAAGCCAGTGGCAAAATCCAT 1076

QY 199 ProAspGluSerPheLysArgGlyLysGluSerAsnLeuValSerThrSerGlnLeuSer 218

DB 1077 -----GAGGCGCATGTCGTAGTACGCGCCGACCATTTTAT 1109

QY 219 Leu----- 219

DB 1110 CTTAAAGCGCTTTCATATATAGACACAGCCCTGCATCTATTCAGGTGATTTTGACACAAAC 1169

QY 220 --MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys 238

Db	1170	TCATTAAACGGCAGACGTCTCTATTATGACAAATCCAAACGAAACCTGCCCAAGGCAA	1229
QY	239	GlnValProAspAspHe-----GlnLeuSerIlePheGluSer	251
Db	1230	TACATCAAAACCAATTGTTGACACTACCAAAAAAGTCATGAACCGATGTATCAAAATT	1289
QY	252	GluAspLys-----GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGly	269
Db	1290	GATGGCAAAATCAACGCGCAACCGCTCTCGGTACGGCCAAATCTTTGGTTAATGACAAAC	1349
QY	270	Leu-----ValProThrLysProProThrProGlyAspPro	281
Db	1350	ACAGAAACCGCACCTTTATCAAAAGACGTGTTCTCCAAAAAGCCAAATCCCAATAACCA	1409
QY	282	ProMetProProAsnGlnProGlnThrThrSerValLeuIleAlaGlyLysTyrAlaIleGly	301
Db	1410	-----AACCTAAT-----	1418
QY	302	AspTyrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer	321
Db	1419	-----TCAGACAGCGTAAAGAGGGGGGTTTATGGTAGCTGGGGCGATGACCTG-----	1466
QY	322	PheGlnAlaIaIaGValPheSerSerAsnAsp-----IleGlyGluArg	335
Db	1467	-----GGGGTAAATTTTATTCCAATGCAACACCATCTATGTGCTTGGTGGTGGTAA	1520
QY	336	IleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSer	355
Db	1521	CGAGCAAAACAGACAAACCTGTGGCCCAAAAAACGGTGTTTATGTAGCGAGCTTTGAA	1580
QY	356	IleAlaGluProIleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGly	375
Db	1581	-----AAACCTAGACACCACTTTGTGGATATGAACAGATTGGCAGATATTATAACAGC	1634
QY	376	LysGlnIleGluAsnProAsnLysGluIleValGlu-----ProTyrSerVal	391
Db	1635	AAAAAGTTAAATGATGCGCGTGTAATGAGAAAAATTGATTAATGTGATATTCTACCAAGTAT	1694
QY	392	GluAlaTyrAsnAspHe-----GluGluPheSerValLeuThrThr	405
Db	1695	GAAAGCGTATGATGATTTCTTGGGGCGAAAAAAGACAAATTACACAAAAAAGTCACG	1754
QY	406	GlnAsn-----TyrAlaLysPheTyrTyrAlaLys	415
Db	1755	AGCAGACCCCAAGCGTCGACGCTATTTTGGCAACATGATTAATTTATATT-----	1808
QY	416	AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro	435
Db	1809	-----AATGGCACTATTATGACCTATACAGCCACAGCACTGTGATTAATTGGCCCTGCGC	1862
QY	436	AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluVal-----	453
Db	1863	GATGCTGTCAAAAGCCAAACCAATCCATTAAGAAAAAATACCTATATGCCACACTAAATAAG	1922
QY	453	-----	453
Db	1923	GACAACCAAGTTACCCGCCATGTCTCTACAGAACCAAGCAATTAAGCCTTAATACCGCC	1982
QY	454	-----LysTyrThrHisIleAla-----GlyArgAspLeuPhe-----	464
Db	1983	ATTGCTGGCAAAAGCTATACAGCATCATGAGTTTGGCGAGCGTGTATACAGTCCAAAC	2042
QY	465	-----LysTyrThrValLysProArgAspThrAspProAspThrPheLeu	479
Db	2043	CAAAACCCCAACGACAGTATTTTGTGCAGAGCGGTAGGCGAGATACACAGCACACGCTG	2102
QY	480	LysHisIleLysLysValIle-----	486
Db	2103	CCCAAGCAGGTAAATTACCTTAACAGAGCTTTGGCGACGCTATCTTAATCCAAAAAAG	2162
QY	487	GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGly-----	501

Db	2163	GACAAAGCTTTAGCAATTAATGAAGAAACCATCAAGAAAAAGGCATCAAGATTACTG	2222
OY	502	LeuThgIuThrGInLeuAlaAlaAlaThrGInLeuAlaIleTyTYrPheTh	519
Db	2223	TTTAACCGGAAGAC-----TTTACCCCGCAAA	2246
OY	520	-----AspSerAlaGInLeuAspLysAspLysLeuAspTYrGInSgluPhe	535
Db	2247	GATGATGACGATGATTTTGACCGCGCATCTGATGATTCACAAAGTAGATGATGCACATGGCGAT	2306
OY	536	GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTYrAlaGInAsp	555
Db	2307	GATGATTTTG-----ATTGCATCTGATGATTCACAAGAT	2339
OY	556	SerAsnProProGInLeuThrAspLeuAspPhePheIleProAsnAsnLysTYrGIn	575
Db	2340	GATGACCGCAGATGGCGGATGACGATGACAGATGATTG-----GGTGATGGTCGACGATAC	2393
OY	576	SerLeuIleGlyThrGInThrGInThrPheAsnProGInAspLeuValAspIleIleArgMetGluAsp	595
Db	2394	GGCGCCGGAGGCAAAAGTGATATCAGTCAAGTAT-----ATTCCGCCCGCATTT	2441
OY	596	LysLysGluValIleProVal-----ThrIAsnLeuThrLeu-----	608
Db	2442	GAATAACAATACTTGCCCATTAATGAAGCCTACTCATGATAAAAAACCTTGGCCTAGATGT	2501
OY	609	-----ArgLysThrValThrGlyLeuAlaGly	617
Db	2502	AAAAATAAGCTAAGCTTGATGTGGATTTTGACACACCAACGCCCTACTGTTAAATTAAAC	2561
OY	618	AspArgThrLysAspPheHisPheGluIleGInLeuLysAsnAsnLysGInGluLeuLeu	637
Db	2562	GATGAGAGAGGTGATATCGTCTGTTGAATATC-----AAAAATGCCAAATTTGATGGCACA	2615
OY	638	SerGInThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIle	657
Db	2616	GGCTTTTACCGCCAAAGCCGATGTGCCAAACTATCTGACAGAGTGGGT-----	2663
OY	658	AsnLeuLysHisGlyGInSerLeuThrLeuGInGlyLeuProGInLysTYrSerTYrLeu	677
Db	2664	AACAACCAAGGTGC-----GGTTTCTTATACAAC	2693
OY	678	ValLysGluThrAspSerGluGlyTYrLysValLysValAsnSerGInGluValAla---	696
Db	2694	ATCAAAAGATATATGATGTCAACGGGCAATTTTGGCACAATAATGGCGAAGGTGGCGAGG	2753
OY	697	-----AsnAlaThrValSerLysThrGly	704
Db	2754	CAGTTACAGTACGAACAAGCGATGGCATCATACACCCCGCAAAAAGCAGGG	2807
RESULT 7			
AAAF28541	ID	AAAF28541 standard; DNA; 49617 BP.	
XX	XX	AAAF28541:	
XX	XX	04-APR-2001 (first entry)	
XX	XX	Genomic fragment #28.	
XX	XX	Genomic library: bacteria; human upper airway; otitis media; sinusitis;	
XX	XX	bronchopulmonary; endocarditis; meningitis; ss.	
XX	OS	Moraxella catarrhalis.	
XX	PN	MO200078968-A2.	
XX	PD	28-DEC-2000.	
XX	PF	16-JUN-2000; 2000MO-US16649.	
XX	PR	18-JUN-1999; 99US-0140121.	
XX	XX		

PA (INCY-) INCYTE GENOMICS INC.
 XX Lagace RE, Patterson C, Berg KL;
 XX WPI: 2001-041427/05.
 XX
 XX Genomic library for identifying diagnostic and therapeutic
 PT compositions, and for identifying virulence factors, regulatory
 PT elements and drug targets, comprises Moraxella catarrhalis nucleic
 acids -
 XX
 XX
 PS Claim 1, page 235-247; 545pp; English.
 XX
 XX The present invention relates to a Moraxella catarrhalis genomic library
 CC comprising of a combination of 41 nucleic acid molecules (see
 CC AAF28514-AAF28534). The library has a number of uses described in the
 CC specification e.g. is useful for identifying diagnostic and therapeutic
 CC compositions. M. catarrhalis (Branhamella catarrhalis) is a large
 CC aerobic, gram-negative diplococcus, normally found among the bacterial
 CC flora of human upper airways. M. catarrhalis is known to cause acute,
 CC localised infections such as otitis media, sinusitis and bronchopulmonary
 CC infection and life-threatening, systemic diseases including endocarditis
 CC and meningitis.
 XX
 XX
 SQ Sequence 49617 BP; 14572 A; 9853 C; 11026 G; 14166 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.0106 Length: 49617
 Score: 177.00 Matches: 164
 Percent Similarity: 33.58% Conservative: 104
 Best Local Similarity: 20.55% Mismatches: 262
 Query Match: 4.49% Indels: 268
 DB: 22 Gaps: 40
 US-09-494-297-2 (1-757) x AAF28541 (1-49617)
 QY 84 TyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluCysSerArgSer 103
 DB 14887 TATTTTGATTAATTTCCCAAAATATCCGATCTG-----CACCTGAAAACGCGAG--- 14937
 QY 104 TyrGlnValTyrCysPheAsnLeuLysLysAla-----PheProLeuGly 118
 DB 14938 -----CATGTGTTGATCTTAATAAAGCAAAATACATCAAAATATATGTTATGTT 14988
 QY 119 SerAspSerSerValLysLys-----TrrTyrLysLysHisAspGlyLeu 133
 DB 14989 GCATTGTGATCACTGCGCAAAACCACTACATGAAATTATACACAAAGCAAAACATC 15048
 QY 134 SerThrLys-----PheGlnuSpTyrAla-----MetSerProArg 145
 DB 15049 AAAAAACAAAACAGCGGATCATTTATCAAAACATTCGTTTGGCTATATGAGCTAAGA 15108
 QY 146 IleThr-----GlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
 DB 15109 GAGCTGAGACCTAAATAAAAAAGGTGACAGACCCAGAGGACAGAACGCTGCATCAT 15168
 QY 160 TyrAsnGly-----HisProGlnAsnAlaAsnGlyIleMetLeuGlyLeu 174
 DB 15169 TTCACCAACCTACTTATTTATTTATCATGTGTGAATGCCAGCACCATCTGCCA----- 15222
 QY 175 GlnProLeuAsnAlaIleArgValThrGlnGlnAlaValTrrTyrTyrSerAspAla 194
 DB 15223 -----AAGCGGATTAATTTGATCATATGAGGCAATGCTGTATCTGACCATGTC 15273
 QY 195 Pro-----IleSerAsnProAspGlu-----SerPhe 203
 DB 15274 AAAAAACGCCCATTTTATGATTAACACAGCATTAAGTAGCAGCACTATTTTAACACACC 15333
 QY 204 LysArgGluSerGlnSerAsnLeuValSerThrSerGlnLeuSerLeu----- 219
 DB 15334 AGAAATATCAATGAAGCGGATTTGGTGAAGTCAGACACATTTATCTAAACGCTTTAA 15393
 QY 220 -----MetArgGlnAla 223

DB 15394 TATAACACACACCCGCCACTTATAGCGTGGACCTTTGATCAAAATACCTTAAGGCAAA 15453
 QY 224 LeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp 243
 DB 15454 TTGTCTTATTTATGACAAACCCAAACAGCAAGACAGCGATGGCGTTATATGAGAGTGC 15513
 QY 244 Phe-----GlnLeuSerIlePheGluSerGlnAspLys----- 254
 DB 15514 TTTGTATACCGACAAAAGGTCAATGATGATGATGATGATGATGATGATGATGATGAT 15573
 QY 255 GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu----- 270
 DB 15574 GGCACACCGCTTACTGGCACACCAACCAATTTGATGATGATTAACACCAATACCCACCT 15633
 QY 271 -----ValProThrLysProProThrProGlyAspProProMetProProAsn 286
 DB 15634 TTTGTTAAAGACCTGTCTCCAAAAGCAATCCCAACACCA-----GACCCCAAC 15687
 QY 287 GlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 306
 DB 15688 -----TCAGATACG 15696
 QY 307 LeuGlnGlyAlaThrLeuGlnLeuThrGlnLysAsnValAsnSerPheGlnAlaArgVal 326
 DB 15697 CTAGAAGCGCGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 15744
 QY 327 PheSerSerAsnAspIle-----GlyGluArgIleGluLeuSer 339
 DB 15745 TTTTATTCCAATGACAGCAACCTTTTGTGCTTTTGTGCTTTTGTGCTTTTGTGCTTT 15804
 QY 340 AspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaLysPro 359
 DB 15805 GAACCTGTGCGCAAAAAGCGGTGATTTTAACT--ACAGATTTGAA-----AAACCC 15855
 QY 360 IleThrPheLysValGlnAlaGlyLysValTyrThrIleLeuAspGlyLys----- 376
 DB 15856 AGCACACGCTTGTGTCGATCAATGACAGAGTGTGTACATTTATGACGCTTAAGTTAAT 15915
 QY 377 ---GlnIleGluAsnProAsnLysGlnIleValGluProTyrSerValGlnAlaTyrAsn 395
 DB 15916 GATGAAAGCAATTAATCAAAATGAGATGAACTGCTGCTGCTGCTGCTGCTGCTGCT 15975
 QY 396 AspPhe-----GluGlnPheSerValLeuThrThr 405
 DB 15976 GAATATTAATTATGACAGACCAACCAACATTCACCAAAAATAAAGCCAGCTCCAA 16035
 QY 406 GlnAsnTyrAla-----LysPheTyrTyr----- 413
 DB 16036 AAAAAACCTGCTTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 16095
 QY 414 -----AlaLys-----AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAla 429
 DB 16096 TTATCAGCGCAAGAAAGCAACAGCTTGTGCTGCTCCAAAGATACCAAGCAACAAATAG 16155
 QY 430 AspLeuLysSerProProAspSerGlnAspGlyGlyLysThrMetThrProAspPheThr 449
 DB 16156 ATTTTGGCTAAATTAACCAAGATGCTC-----AAAGTAAGCAGACATTAAGTT 16203
 QY 450 Thr----- 450
 DB 16204 ACCAAATTCGTTCTACAAACCAACCAAGTAAGCCGTATACCGCATTCATGCCAAAAGC 16263
 QY 451 -----GlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
 DB 16264 TATGACCAACATCAGTTTGTGTAAGTATTTGATGATTAACAAAGCAACCAACACAGC 16323
 QY 465 LysTyrThrValLysProArgAspThrAspProAspThrPheLeuLys----- 480
 DB 16324 AGTTATTTTGTCAAGCGGCTCAAGCGGATGTCAGTACTACACCTGCCAGTGCAGGTAA 16383
 QY 481 -----HisIleLysValIleGluLysGlyTyrArg 491

```

Db 16384 TTCACCTATATAGCTCTTTGGGCGAGCTGACCCAGAAAAAGACAAAGTTATAGC 16443
QY 492 GltuysglylnalalegluTySerGlyLeuThrgluThrgluInleuArgAlaIaIaThr 511
Db 16444 AAGATAGGATACCATCAACCAAAAAGGCTTTAAAGAT----- 16482
QY 512 GlnleuAlaIeTyTyThrThr-----AspSerAlaIaIaIaIaIaIaIaIaIa 524
Db 16483 -----TATATATTGACCAAAAGACTTTATCCACAGATGACGATGACGATGAC 16530
QY 525 AsplysAsplysLeu-----LysAspTyThsGlyPheGly 536
Db 16531 GATGACCATGATGTTGACCGCATGATGATGATGATGATGATGATGATGATGATGAT 16590
QY 537 AspmelaAspSerThrLeuAlaValAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 556
Db 16591 GATTTC-----ATTGCACTGATGATGATGATGATGATGATGATGATGATGAT 16623
QY 557 AsnProProGlnleuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyGlnSer 576
Db 16624 GAGCAGATGCGCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16677
QY 577 LeuIleGlyThrglnThrglnPheIleProGluAspLeuValAspIleIleArgMetGluAspLys 596
Db 16678 GCCGCGAGCAAAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16725
QY 597 LysGluValIleProVal-----ThrHisAsnleuThrLeu----- 608
Db 16726 AACAAATACCTGGCCATTATGAGCCATCATGATGATGATGATGATGATGATGATGAT 16785
QY 609 -----ArgLysThrValThrglyLeuAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 618
Db 16786 AATAAGGCTAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16845
QY 619 ArgThrLysAspPheHisPheGlnIleGlnLeuLysAsnLysGlnGlnLeuLeuSer 638
Db 16846 GAGAGAGGATGATGCTCTTTGATATC-----AAAAAGGCAAAATGATGATGATGATGATGAT 16899
QY 639 GlnThrValLysThrAspLysThrAsnLeuGlnPheLysAspGlyLysAlaIaIaIaIaIaIa 658
Db 16900 TTATACCGCCAAAGCGATGCGCAAACTATGCGCAAAAGTGGCT-----AAC 16947
QY 659 LeuLysHisGlyGlnSerLeuThrLeuGlnGlyLeuProGlnGlyTySerTyLeuVal 678
Db 16948 AACCAAGGTGC-----GTTTCTTATACAAATC 16977
QY 679 LysGlnThrAspSerGlnGlyTyTyLysValLysValAsnSerGlnGlnValAlaIaIa 696
Db 16978 AAGATATTGATGTTAAGGGCAATTTTGGCACAAATGCGCAAGAGTTGGCA 17031

```

RESULT 8
AAV82021 standard; DNA; 2718 BP.

```

XX AAV82021:
XX
AC 21-JUN-1999 (first entry)
XX
DE Moraxella catarrhalis VH19 lbpB gene.
XX
KM Lactoferrin receptor; lactoferrin binding protein; LBp1, LBp2;
KM lbpA gene; lbpB gene; ORF3; infection; otitis media; sinusitis;
KM conjunctivitis; pneumonia; bronchitis; tracheitis; emphysema;
KM diagnosis; therapy; vaccine; Branhamella catarrhalis, ss.
XX
XX Moraxella catarrhalis.
OS
FH Key Location/Qualifiers
FT CDS 1..2718
FT /tag= a
FT /transl_except= (pos:844..846, aa:Thr)
FT /transl_except= (pos:847..849, aa:Thr)
FT /transl_except= (pos:850..852, aa:Thr)

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PT /transl_except= (pos:853..855, aa:Thr)
PT /transl_except= (pos:856..858, aa:Thr)
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PT /transl_except= (pos:892..894, aa:Thr)
PT /transl_except= (pos:895..897, aa:Thr)
PN W09855606-A2.
PD 10-DEC-1998.
XX
XX 02-JUN-1998; 98WO-CA00544.
XX
XX 08-MAY-1998; 98US-0074658.
XX
XX 03-JUN-1997; 97US-0867941.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;
XX WPI: 1999-070266/06.
XX P-PSDB: AAW89421.
XX
XX Lactoferrin receptor genes from Moraxella, especially M. catarrhalis
XX - useful to diagnose Moraxella infection e.g. to detect otitis media
XX due to M. catarrhalis infection and to immunise against such
XX infections
XX
XX Claim 8; Fig 16a-O; 202pp; English.
XX
XX This polynucleotide comprises the lactoferrin binding protein lbpB
XX gene of Moraxella catarrhalis (Branhamella catarrhalis) strain VH19.
XX It encodes lactoferrin binding protein 2 (lbp2, see AAW89421). The
XX genes and DNA sequences of the lactoferrin receptor (lfr) locus of
XX Moraxella are useful for diagnosis, immunisation, and the
XX generation of diagnostic and immunological reagents. Immunogenic
XX compositions, including vaccines, based upon expressed recombinant
XX lbp1 and/or lbp2 and/or ORF3, portions of these, or their
XX analogues, can be prepared for prevention of diseases caused by
XX Moraxella. M. catarrhalis is a causative agent of otitis media and
XX has been associated with sinusitis, conjunctivitis and inflammatory
XX diseases of the lower respiratory tract, such as pneumonia, chronic
XX bronchitis, tracheitis and emphysema.
XX
XX Sequence 2718 BP; 958 A; 585 C; 547 G; 628 T; 0 other;
SQ

```

Alignment Scores:

```

Pred. No.: 0.000348 Length: 2718
Score: 176.00 Matches: 164
Percent Similarity: 33.42% Conservative: 102
Best Local Similarity: 20.60% Mismatches: 264
Query Match: 4.46% Indels: 266
DB: 20 Gaps: 40

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US-09-494-297-2 (1-757) x AAV82021 (1-2718)

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QY 84 TyrTyTyLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGlnGlySerArgSer 103
Db 493 TATTTGATAAATTCGCCAAATAATCCGATCTG-----CACCTAGAAAAACAGCGAG--- 543
QY 104 TyrGlnValTyrcysPheAsnLeuLysAla-----PheProLeuGly 118
Db 544 -----CATGTGTTGATGCTAAAAAAGCAATACATCAAAATATATGTTATGCT 594
QY 119 SerAspSerSerValLysLys-----TrpTyTyLysLysHisAspGlyTle 133

```

Db 595 GCATTGTCATCACCCTGCCAATAAACCAACCTACATGATTTATCAACAAGAACAAACATC 654
 QY 134 SerThrIys-----PheGluAspTyrAla-----MetSerProArg 145
 Db 655 AAAAAACAAACCAAGCGATGATATCAAAACATTCGTTTGGCTATATGACCTAGA 714
 QY 146 IleThr-----GlyAspLeuAsnGlnIleuArgAlaValMet 159
 Db 715 GAGCTGACCTAAATATAAAGGTGACAGACCCAGACGACAGAACCGTGGCATCTT 774
 QY 160 TyrAsnGly-----HisProGlnAsnAlaAsnGlyIleMetGluGlyLeu 174
 Db 775 TTCACCAACACTACTTATTTATCATGAGAGATGCGACACCACTTCGCCA----- 828
 QY 175 GluProLeuAsnAlaIleArgValThrGlnGluAlaValTyrTyrTyrSerAspAsnAla 194
 Db 829 -----AAGGGGGTAAATTTGACTATGAGGCAATGGTGTATCTGACGATGTC 879
 QY 195 Pro-----IleSerAsnProAspGlu-----SerPhe 203
 Db 880 AAAAAACGCCCATTTTATGATTAACAGACGATTAAGTACGACTTATTTAACTCAACC 939
 QY 204 LysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu----- 219
 Db 940 AGAAATCAATATGAAGCGATTTGTGAGTCACACACATTTATCTAAACAGCTTAA 999
 QY 220 -----MetArgGlnAla 223
 Db 1000 TATTAACACACCCCGCCACTTATAGCGTGACCTTGATCAAAATACCTTAAAGGCATA 1059
 QY 224 LeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp 243
 Db 1060 TTGCTTATATATGACAAACCCAAACAGACCAACCCGATGGCGTATATATGAGATCAG 1119
 QY 244 Phe-----GlnLeuSerIlePheGluSerGluAspLys----- 254
 Db 1120 TTTCATACCGCAAAAGTCAATGAAGCGATGCTATATGATTAAGCCCAAGATTAA 1179
 QY 255 GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu----- 270
 Db 1180 GGCACACGCTTACTGCGACAGCCAAATCTTGTATGATGATTAACACCAATACCGCACT 1239
 QY 271 -----ValProThrLysProProThrProGlyAspProPrometProProAsn 286
 Db 1240 TTTCGTTAAAGAGCTGTTCTCCAAAAAACCAATCCCAACACCA-----GACCCCAAC 1293
 QY 287 GlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 306
 Db 1294 -----TCAAGTACG 1302
 QY 307 LeuGlnGluAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgVal 326
 Db 1303 CTAAACAGCGGCTTTATGTGATGCGGCGATGAGCTG-----GCGGGTAA 1350
 QY 327 PheSerSerAsnAspIle-----GlyGluArgIleGlnLeuSer 339
 Db 1351 TTTTATCAATATGACAAACGCAACTTTGTGCTCTTGGTGGCAACAGACAAACGACC 1410
 QY 340 AspGlyThrTyrThrLeuThrGlnLeuAsnSerProAlaGlyTyrSerIleAlaGluPro 359
 Db 1411 GAACCTGCGCCACAAAAACGGTGTATTTAGT---ACAGGATTTCGA-----AAACCC 1461
 QY 360 IleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGlyLys----- 376
 Db 1462 AGCCACGAGCTTTGTGGCAATGAAGATGTGTCATTTATGACGTTAAAAAGTTAAAT 1521
 QY 377 ---GlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsn 395
 Db 1522 GATGATCAATATATCAATTAATGAAGTAAACTGCTCCCTGATTAATAAAGAAATTTAT 1581
 QY 396 AspPhe-----GluGluPheSerValLeuThr 405
 Db 1582 GAATATATATATGACAGACCCAAACAAATTCACAAAAAATAAACGCCAGCGTCCAA 1641

QY 406 GlnAsnTyrAla-----LysPheTyrTyr----- 413
 Db 1642 AAAAAACCTGCTTATTTTGGTACACATGATGATTTTATTTATGATGATTAATGAC 1701
 QY 414 -----AlaLys-----AsnLysAsnLysSerGlnValValTyrCysPheAsnAla 429
 Db 1702 TTATCAGCCAAAGAAAGCAACAAACAGCTTGCTCTCCCAAGTACCAGACCAATTAAGAGT 1761
 QY 430 AspleuLysSerProProAspSerGluAspGlyLysThrMetThrProAspPheThr 449
 Db 1762 ATTTTGGCTAAATACCCAGATGCC-----AAAGTACACACAGCAATTAAGATT 1809
 QY 450 Thr----- 450
 Db 1810 ACCAAATCGTTTACAAACAGCCAAAGATTAAGCCGATTAACGCCATTCATGCCAAAAAGC 1869
 QY 451 -----GlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
 Db 1870 TATGACACATCAGTTTGGTGAAGTATTTGATATGATTAACAAAGGCAACCCACACGCC 1929
 QY 465 LysTyrThrValLysProArgAspThrAspProAspThrPheLeuLys----- 480
 Db 1930 AGTTATTTTGTCAAGCGGTCAGACGGATGCTACTGACGTGCCAGTCAGGTAA 1989
 QY 481 -----HisIleLysValIleGluLysGlyTyrArg 491
 Db 1990 TTCACATATAATGCTTTGGGACGAGCTGACCCGAAAAAGCAAAAGGTTATATGAC 2049
 QY 492 GluLysGlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgAlaIleThr 511
 Db 2050 AAAGTGAAGTACCATCAACCAAAAGCTTTAAAGT----- 2088
 QY 512 GlnLeuAlaIleTyrTyrPheThr----- 519
 Db 2089 -----TATATATGACCAAGACTTATCCCAAGATGACGATGACATGAC 2136
 QY 520 AspSerAlaGluLeuAspLysAspLysLeuLysAsp---TyrHisGlyPheGlyAspMet 538
 Db 2137 GATGATTTGACCGCATGATGATGATCAACAGATGATTAATACAGGATGATGATTTG 2196
 QY 539 AsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnPro 558
 Db 2197 -----ATTCACTGATGATTTACACAGATGATGACACA 2229
 QY 559 ProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIle 578
 Db 2230 GATGCGCATGACGATTCAGATGATTTG-----GGTATGTCGACAGATGACGCCGCA 2283
 QY 579 GlyThrGlnTyrPheIleProGluAspLeuValAspIleIleArgMetGluAspLysGlu 598
 Db 2284 GGCAAAGCTGATCATGACGATTAAT-----ATTCGCTGATTTGAAACAA 2331
 QY 599 ValIleProVal-----ThrHisAsnLeuThrLeu----- 608
 Db 2332 TACTTGCCCATTAATGACCTTACTCATGAATAAACCTTTGCCCTAGATGTAATAATTAAG 2391
 QY 609 -----ArgLysThrValThrGlyLeuAlaGlyAspArgThr 620
 Db 2392 GCTAAGTTTGAATGAACCTTGCACACACAGCCCTAAGCTTAATTAACGATGACAGCA 2451
 QY 621 LysAspPheHisPheGluIleGluLeuLysAsnLysGlnGluLeuLeuSerGlnThr 640
 Db 2452 GGTATATTCGCTTTGATATC-----AAAAATGCAAAATTAATGGCAGCATTTAAC 2505
 QY 641 ValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLys 660
 Db 2506 GCCAAAGCGATGCGCAACACTATCGTGAAGAAAGTGGT-----AACACCAA 2553
 QY 661 HisGlyLysLeuThrLeuGlnGlyLeuProGluLysTyrSerTyrLeuValLysGlu 680
 Db 2554 GCTGCG-----GGTTCTTATACACATCAAGAT 2583

QY 681 ThrAspSerGluGlyTyrLysValLysValAsnSerGlnIValAla 696
||| ::|||
DB 2584 ATTGATGTTAAGGGGCAATTTTGGCACAAATGGCAAGATTGGCA 2631

RESULT 9
AB069442
ID AB069442 standard; DNA; 4161 BP.
XX
AC AB069442:
DT 29-AUG-2002 (first entry)
XX
DE Listeria innocua DNA sequence #881.
XX
KM Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
OS Listeria innocua.
XX
PN W0200228891-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-FR03061.
XX
PR 04-OCT-2000; 2000FR-0012697.
XX
PA (INSP) INSP PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
PI Kunst F, Glaser P.
XX
DR WPI; 2002-332479/37.
XX
PT New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators
PS
XX
XX Claim 7: SEQ ID 2255; 180bp; French.

CC The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 4161 BP; 1660 A; 657 C; 815 G; 1029 T; 0 other;

Alignment Scores:
Pred. No.: 0.00888 Length: 4161
Score: 161.00 Matches: 163
Percent Similarity: 34.98% Conservative: 127
Best Local Similarity: 19.66% Mismatches: 301
Query Match: 4.08% Indels: 238
DB: 24 Gaps: 41

US-09-494-297-2 (1-757) x AB069442 (1-4161)

QY 10 LeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSerLys---ArgPheThrVal 28
||| ::|||
DB 988 CTCAGTAGCTTTCATACAAAAAAGTACATATATGACAAAGCATGTTAGATATTCGAA 1047

QY 29 ThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSerMetValGlyAlaLys 48
::: |||
DB 1048 AGCTGACAAAGCTTAAATATACAGCACTTTTGAAGCAATAGTCTTACAACTGAATGAAG 1107

QY 49 ThrValPhe-----GlyLeuValGlu----- 55
||| ::|||
DB 1108 TTATGTTTACCGAGCCAAATTAATTGTCCTCATTAATAGTTAGCAAAAAAATAAGTTT 1167

QY 56 -----SerSerThrProAsnAlaIleAsnProAspSerSerGluTyrArg--- 71
::: |||
DB 1168 TATACGTGGCTACGATGAAATAAAGTTTAATTCACCCCGCAGTCACCTTATTAATGCA 1227

QY 72 ---TrpTyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrTyrLysGlnPheArgVal 90
|||
DB 1228 ACGTGG-----ACGACCCCTCGTACAAACGACAAATTTGG 1263

QY 91 AlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAsn 110
::: |||
DB 1264 TCAGACTCTTTAAGCATGAAATACGACGGTGCACCATGATGATATATCATTTGGTCT 1323

QY 111 LeuLysLysAlaPheProLeuGlySerAspSerVal-----LysLysTrpTyr 127
::: |||
DB 1324 GCTGTAAATTAATATC---ATAGCCATTTGATCTAATTTATTCAGGTGATGCTGAAA 1380

QY 128 LysLysHisAspGlyLysSerThrLysPheGluAspTyrAlaMetSerPro----- 144
::: |||
DB 1381 GCTGAGGATTAATTTTATTCAGCACAGCATTAAGATTTCAATCTATGATTTCCGCTG 1440

QY 145 ---ArgIleThrGly-----AspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsn 161
::: |||
DB 1441 GTACAGCATACAGATCCGATAGTACTACGACACCTGGTGAATATGAAATACATATATG 1500

QY 162 GlyHisProGlnAsnAlaAsnGlyIleMetGlyGlyLeuGluProLeuAsnAlaIleArg 181
::: |||
DB 1501 -----GTAAATGGCTTGACATCAATCAATCAGTACCA 1533

QY 182 ValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGlu 201
||| ::|||
DB 1534 GTCAAAAGAAATATACCAAGTCTTTAGCGGAAATCACTATCTATACA---AAAGAA 1590

QY 202 SerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArg 221
||| ::|||
DB 1591 TCCTGGAAA-----GCCGAAGATTAATTTGTTTCAGCAACCAAT-----AAAAA 1635

QY 222 GlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValPro 241
::: |||
DB 1636 GGTAAATATTCAGATATTTCTGTCAGTACCGTACAGGGGAGATGATGTAATATACACA 1695

QY 242 AspAspPheGlnLeu----- 246
||| ::|||
DB 1696 GAGACTACCAATTTATGATATACATTTGATGAGCTCTACAAATAATTTGACGGGTG 1755

QY 247 -----SerIlePheGluSerGluAspLys-----GlyAspLysTyr 258
||| ::|||
DB 1756 AAAGAGATTAAGCATATAGCAAGCTAAAGATTCAATCTTATATAGTGTATAGCTGG 1815

QY 259 AsnLys-----GlyTyrGln 263
|||
DB 1816 AATTCCAAGACATTTTATTTTCAGCGACAGATTAAGATGTATATCCGGTGACCTTAAG 1875

QY 264 AsnLeuLeuSerGlyLysLeuValProThr---LysProProThrProGlyAspPropo 282
::: |||
DB 1876 GATATTAAGTATACAGCACAGTAAACAGATTAACAGCAAGTAAACAAAGTATACGTAT 1935

QY 283 MetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAsp 302
::: |||
DB 1936 TTGTATGAAACCAAGTAAAGAGTACCATTAACATCAAA-----CGCGAT 1983

QY 303 TyrSerLysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPhe 322
||| |||
DB 1984 CAATCAACTTTAAGGCCCAAGATTCATATTTATATACGAGATATGAGTAAAGTGCAAA 2043

QY 323 GlnAlaArgValPheSerSerAsnAspIleGlyGluArgIleGluLeuSerAsp----- 340
::: |||
DB 2044 GACAAATTTATACAGCCACAGATTAAGATGTAATCCAGTACATTTAAGATATATGAA 2103

QY 341 -----GlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGlu 358

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Db      2104 GTCCAGGCTACGACAGACACA-----AAA 2130
Qy      359 ProIleThrPheLysValGluAlaGlyValTyrThrIleIleAspGlyLysGlnIle 378
Db      2131 CCAGCAACTAACCAAGATT-----ACGTATATATATGGA----- 2163
Qy      379 GluAsnProAsnLysGluIle-----ValGluProTyrSerValGluAla 393
Db      2164 ---AATCTAAGTAAAGAAAGTTACCGTAACAGCAAGCAACTTTTAAGACC 2220
Qy      394 TyrAsnAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyr 413
Db      2221 ---AAAGATTCAGCTCTTATGATAGTGATACGCGAATCCAAAGATATTTTATTC 2277
Qy      414 AAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSer 433
Db      2278 GCAACCGCATTAAGATGGC-----ACT 2298
Qy      434 ProProAspSerGluAspGlyGlyLysThrMetThrProAspPheThr---ThrGlyGlu 452
Db      2299 CCACTAGACTTTAAGATATATAAGTCGACGACACAGTAGACACCCAGCAAGCAAGAACT 2358
Qy      453 ValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAsp 472
Db      2359 AACAGGTAACTCTATTTGTATGAAACCAAGTAAGAAAGTACCGTAAGCTCAA--- 2415
Qy      473 ThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGlu 492
Db      2416 GCGGATCAACACACTTA-----GAG 2436
Qy      493 LysGlyGlnAlaIleGluTyrSerGly-----LeuThrGluThrGluLeuArgAla 509
Db      2437 GTCAAAGATTGATATTATTATTAAGTGAAGCAAGTGAAGCAAGATTAATTATTC 2496
Qy      510 AlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeu 529
Db      2497 GCCACA-----GACCAAAACC 2511
Qy      530 LysAspTyrHisGlyPheGlyAspMetAsn-----AspSerThrLeuAla 544
Db      2512 GGAATTCAGTACGCTTAAAGCATATTAAGTCGAGCTACAGTACAGCAACCAAGCA 2571
Qy      545 ---ValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProGluLeuThr--- 562
Db      2572 GGAACATAACAGGTTACCTATACGTAATCAATCAACAGGAAGTTACATACACATC 2631
Qy      563 -----AspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeu 577
Db      2632 AAACCGCATCAAGCACTTACAA-----GCCAAAGATTCAATT 2670
Qy      578 Ile-----GlyThrGlnTyrHisProGluAspLeuValAspIleIleArgMetGluAsp 595
Db      2671 ATTATATACCGGATGATGCGAAAGCAGAGAAC-----AACTTATTTCCGCTACTGAT 2724
Qy      596 LysLysGluValIleProValThrHisAsnLeuThrLeuAlaGlyLysValThrGlyLeu 615
Db      2725 AAACGAGAAAGACAATTGACTTTAAATAATTAAAGTGAAGGACGACATA----- 2775
Qy      616 AlaGlyAspArgThrLysAspPheHisPheGluIleGluLeu----- 629
Db      2776 -----GATACCACAAAAAGCTGTAATTATGACATCACTTTCTTATTCAGAGTCACT 2829
Qy      630 ---LysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeu 648
Db      2830 CGTAGTACTGAATTGATTAACATTAATTAACATCACTTAATTAATTAATTAATTAATTA 2889
Qy      649 GluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyLysSerLeuThrLeuLys 668
Db      2890 GAACGAAAGACTCACT----- 2907
Qy      669 GlyLeuProGluGlyTyrSerTyrLeuValLysGlu-----ThrAspSer 683

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Db      2908 ---CTTATGAAGAGACAGATGATACGTAAGATTAACCTTTGTTTCAGCAACGATAAA 2964
Qy      684 GluGlyTyrLysValLysValAsnSerGlnGluValAlaAsnAla----- 698
Db      2965 GATGGCAATACAGTGAAGCTTTAAAGCTTATGAGTTAAAGAACTGTAATACCAAAA 3024
Qy      699 -----ThrValSerLysThrGlyIleThrSerAspGluThrLeuAla 712
Db      3025 GCAGCACTTACAAATATCACCATTATATGAGGATCAGCAGATCAGCAATTAACAGTGACA 3084
Qy      713 PheGluAsnAsnLysGluProValVal 721
Db      3085 GTTACGCCAATCAACAACTAAATCGTA 3111

RESULT 10
AB067871
ID      AB067871 standard; DNA; 4185 BP.
XX      XX
AC      AB067871;
XX      XX
DT      29-AUG-2002 (first entry)
XX      XX
DE      Listeria innocua DNA sequence #673.
XX      XX
KW      Antibacterial; Listeria; food contamination; mutational analysis;
        infection; ds.
OS      Listeria innocua.
XX      XX
PN      WO200228891-A2.
XX      XX
PD      11-APR-2002.
XX      XX
PF      04-OCT-2001; 2001WO-FR03061.
XX      XX
PR      04-OCT-2000; 2000FR-0012697.
XX      XX
PA      (INSP ) INST PASTEUR.
XX      XX
PI      (CNRS ) CNRS CENT NAT RECH SCI.
XX      XX
PT      Kunst F, Glaser P;
DR      WPL: 2002-332479/37.
XX      XX
PT      New genomic sequences from Listeria species, useful for detection,
        treatment and prevention of infection, also related polypeptides,
        antibodies and modulators
XX      XX
PS      Claim 7; SEQ ID 684; 180pp; French.
XX      XX
CC      The present invention relates to nucleic acid sequences
        (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
        and primers for identification and/or detection of Listeria (e.g. as
        contaminants in foods, or mutational analysis) and for analysis of
        gene expression. Proteins encoded by the nucleic acid sequences can be
        used to screen for compounds that modulate gene expression, replication
        and pathogenicity of Listeria (potential therapeutic agents), also for
        treating infections by Listeria, and are useful as immunogens in
        anti-Listeria vaccines.
CC      Note: The sequence data for this patent did not form part
        of the printed specification, but was obtained in electronic format
        directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX      XX
SQ      Sequence 4185 BP; 1671 A; 658 C; 821 G; 1035 T; 0 other;

Alignment Scores:
Pred. No.: 0.00894      Length: 4185
Score: 161.00      Matches: 163
Percent Similarity: 34.98%      Conservative: 127
Best Local Similarity: 19.66%      Mismatches: 301
Query Match: 4.08%      Indels: 238
DB: 24      Gaps: 41

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QY 630 ---LysAsnAsnLysGlnLuleuSerGlnThrValLysThrAspLysThrAsnLeu 648
 Db 2854 CGTACTGACTGATTTAGTAAACAACTTACAGTACAGTCAAAAAATCACTAACTTG 2913
 QY 649 GlnPheLysAspGlyLysAlaThrIleAsnLeuLysHISgLySerLeuThrLeuGln 668
 Db 2914 GAAGCAAAAGACTCAACT----- 2931
 QY 669 GlyLeuProGlyLysThrSerTyrLeuValLysGlu-----ThrAspSer 683
 Db 2932 ---CTTATGAAAGGACAGACAGTACCTAAAGTAACTTTGTTTCAGCAACCATTA 2988
 QY 684 GlnGlyTyrLysValLysValAsnSerGlnGluValAlaAsnAla----- 698
 Db 2989 GATGCAATACAGTGGACTTTAAAGCTATTGAGTTAAAGCACTGTAATACCAAAA 3048
 QY 699 -----ThrValSerLysThrGlyIleThrSerAspGlnThrLeuAla 712
 Db 3049 GCAGCACTTACAAAATCACCTATTCATATGCAGCATCAGCAACAACTTACAGTACA 3108
 QY 713 PheGlnAsnAsnLysGlnProValVal 721
 Db 3109 GTCTAGCCAACTCAAACTAAATCCTA 3135

RESULT 11
 AAX20201
 ID AAX20201 standard; DNA; 4249 BP.

XX AC AAX20201;
 XX DT 20-APR-1999 (first entry)
 XX DE Enterococcus faecalis EF104 gene fragment.
 XX KM Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
 XX KM detection; attenuation; antigenic; ss.
 XX OS Enterococcus faecalis.
 XX PN W09850554-A2.
 XX PD 12-NOV-1998.
 XX PE 04-MAY-1998; 98WO-US08959.
 XX PR 14-NOV-1997; 97US-0066009.
 XX PR 06-MAY-1997; 97US-0044031.
 XX PR 16-MAY-1997; 97US-0046555.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Bailey C, Choi GH, Hiromocky J A, Kunsch CA;
 DR WPI: 1999-070095/06.
 DR P-PSDB: AAY00211.
 PT New isolated Enterococcus faecalis polynucleotides - used to develop
 PT products for the detection of Enterococcus and for use in vaccines
 PT for prevention or attenuation of Enterococcus infection
 PS Claim 1: Page 202-203; 301pp; English.
 CC The present sequence encodes an antigenic polypeptide fragment
 CC isolated from Enterococcus faecalis. The present invention describes
 CC genes, proteins and antigenic polypeptides isolated from E. faecalis.
 CC The proteins can be used in vaccines for preventing or attenuating an
 CC infection caused by a member of the Enterococcus genus in an animal.
 CC They can also be used for detecting Enterococcus antibodies in a sample.
 CC The nucleotide sequences can be used for detecting Enterococcus nucleic
 CC acids. Products from the present invention can also be used for
 CC screening compounds to identify agonists and antagonists of E. faecalis
 CC protein activity.
 XX

SQ Sequence 4249 BP; 1579 A; 779 C; 815 G; 1069 T; 7 other:
 Alignment Scores:
 Pred. No.: 0.00911 Length: 4249
 Score: 161.00 Matches: 159
 Percent Similarity: 34.83% Conservative: 104
 Best Local Similarity: 21.06% Mismatches: 326
 Query Match: 4.08% Indels: 166
 DB: 20 Gaps: 40
 US-09-494-297-2 (1-757) x AAX20201 (1-4249)
 QY 39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56
 Db 1451 TCATTAGTACACCTGTAAATGGCTCTAATAAGCCATTCAATTAGTATCCGATCAATAT 1510
 QY 57 ---SerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTyrGlyTyr 75
 Db 1511 ATTGAAACCAATTAGCTGTATTATTCCT---TTGAATGCTGAACAGCTGGGCTAATTAT 1567
 QY 76 GluSerTyrValArgGlyHisProTyrTyrLysGlnPheArgValAlaHisAspLeuArg 95
 Db 1568 GATCAA-----AATGTCCTATTCATCAAGA 1594
 QY 96 -----ValAsnLeuGlyLysArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113
 Db 1595 ACACTGCTCAGTATGAGGACCAAGCAAGCAACCGAATTCMAATTGAAATTAAAGTA 1654
 QY 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrTyrLysLys 129
 Db 1655 AAGCATCCTAATTATCTTTCATTACGACTCAAAAGAAATTAATTATTTATTAACAAG--- 1711
 QY 130 HisAspGlyLysThrLysPheGlyAspTyrAlaMetSerProArgIleThrGlyAsp 149
 Db 1712 -----TTAGAACG-----GATTATACGTAACCCCAACGTCAAGATGTTCA 1753
 QY 150 GluLeuAsnGlnLysLeuArgAlaValIleMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169
 Db 1754 GTTATTAAAGTTCACAGCCCAATTAACAGCAAGAAATTCMAATTCGTTTATTAATTAT 1813
 QY 170 IleMetGlyLysLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
 Db 1814 GTGCCAGATAGTGTCCCAAAAGATAAAGTATCCAGTCGATACGATACCGATACAGTATG 1873
 QY 185 GluAlaValTyrPyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
 Db 1874 AGTGGTGAAGTTTAACTCCAGTTGATGACGACGATTAAGTACTACT-----AATGTAAG 1924
 QY 205 ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
 Db 1925 CGTGGTCTGAAACGAACTTCAAAGTAAAGTAAATTCATTCCTTGTCATAGCAGCAAT 1984
 QY 225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
 Db 1985 GATTCCTTTGACTCACTAAGCGTCCGTCAAAAATTCACGCGGCC-----GATGTT 2038
 QY 245 GlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264
 Db 2039 CTTTGTGACATTATGATGATTTCAAC-----GATCAGGATGATCAATTAATTCACAA 2092
 QY 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPheMetPro 284
 Db 2093 TACTGGAGCCGGGCAATCTTGTGATTAACCAATGACGCCCAACAGCCCTGGATATGCA 2152
 QY 285 -----ProAsnGlnProGlnThrThrSerValLeuIle-----Arg 296
 Db 2153 ACGATTACTTTGACGAAATAACCAATAGTATACAGCTTGATTTGGAAAAACCAAGAA 2212
 QY 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGlnGlyAlaThrLeuGln 313
 Db 2213 CGTTACATTATTT---GAGTATAAAAACCCCAATGCTGATGCTGCAACTCTTTAT 2269
 QY 314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327

Db	2270	ATTAACAGGACAGCAAGAAAGCCAAATCGAATTAATTAATGAAGGCTCTGCTTCGTTCT	2322	ATTAACAGGACAGCAAGAAAGCCAAATCGAATTAATTAATGAAGGCTCTGCTTCGTTCT	2322
Oy	328	SerSerAsnAspIleGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu	347	SerSerAsnAspIleGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu	347
Db	2330	GTTCAAAAT-----GAAGCGTTAGACATTGTTGAGTCGAACA-----	2365	GTTCAAAAT-----GAAGCGTTAGACATTGTTGAGTCGAACA-----	2365
Oy	348	LeuAsnSerProAlaGlyTyrSerIleLeuGluProIleThrPheLysValGluAlaGly	367	LeuAsnSerProAlaGlyTyrSerIleLeuGluProIleThrPheLysValGluAlaGly	367
Db	2366	-----CAAGCGGCGAATCCACATTTAAAAATGTAAACAAAACG	2404	-----CAAGCGGCGAATCCACATTTAAAAATGTAAACAAAACG	2404
Oy	368	LysValTyrThr-----IleLeuAspGlyLys-----GlnIleGluAsnProAsnLysGlu	384	LysValTyrThr-----IleLeuAspGlyLys-----GlnIleGluAsnProAsnLysGlu	384
Db	2405	ACAGTAACACAAAAAATATTGATATATAAAACACATCGCTGTGAAAAATCCACAGCTTAA	2466	ACAGTAACACAAAAAATATTGATATATAAAACACATCGCTGTGAAAAATCCACAGCTTAA	2466
Oy	385	IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThr	404	IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThr	404
Db	2465	TTAACACCAAAAGGACCAACCAACGCTCAATTCGATTGAATTTCATTACCGTG-----	2518	TTAACACCAAAAGGACCAACCAACGCTCAATTCGATTGAATTTCATTACCGTG-----	2518
Oy	405	ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal	424	ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal	424
Db	2519	-----AAAGCGGTCACCAAGAGATGCT	2533	-----AAAGCGGTCACCAAGAGATGCT	2533
Oy	425	TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMet	444	TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMet	444
Db	2540	TAT-----TCATTAGAGAGACTACAAACGGTCCGAAATCTCAT	2578	TAT-----TCATTAGAGAGACTACAAACGGTCCGAAATCTCAT	2578
Oy	445	ThrProAspPheThrThrGlyLys-----ValLysTyrThrHisIleAlaGlyArg	461	ThrProAspPheThrThrGlyLys-----ValLysTyrThrHisIleAlaGlyArg	461
Db	2579	TTTAAAGCTCTATACCTTTCACAGAAAACATTACGATGTGAATACATACGCTCTCTCAAC	2633	TTTAAAGCTCTATACCTTTCACAGAAAACATTACGATGTGAATACATACGCTCTCTCAAC	2633
Oy	462	AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis	481	AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis	481
Db	2639	GCTGGCCAAATCTATACAGAAAACAAATCGACTCGTAACATTTGAACCAAGATGCTGCT	2698	GCTGGCCAAATCTATACAGAAAACAAATCGACTCGTAACATTTGAACCAAGATGCTGCT	2698
Oy	482	IleLysLysValIle-----GluLys	488	IleLysLysValIle-----GluLys	488
Db	2699	AGCAAGAAAAGATCCACCGCCCAATCAATTTCTCAGAAAGTGATCGGAA	2758	AGCAAGAAAAGATCCACCGCCCAATCAATTTCTCAGAAAGTGATCGGAA	2758
Oy	489	GlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnThrGlnLeuArg	508	GlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnThrGlnLeuArg	508
Db	2759	GGTATGTTGTTTATTAAGCAACTGCCACATTTCTACACGCCTAAACGTAGAGAGATGAACCA	2818	GGTATGTTGTTTATTAAGCAACTGCCACATTTCTACACGCCTAAACGTAGAGAGATGAACCA	2818
Oy	509	AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerAlaGluLeu	524	AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerAlaGluLeu	524
Db	2819	GCAATTCGGAAGTTCTTTGACACTAATGTATATGTCACGCATACAGCAACGCAATTT	2878	GCAATTCGGAAGTTCTTTGACACTAATGTATATGTCACGCATACAGCAACGCAATTT	2878
Oy	525	AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet--AsnAspSerThrLeu	543	AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet--AsnAspSerThrLeu	543
Db	2879	ACAACAGATGAAAGAGTCACTCTGATGCGCATCAACAGGAGTAATTAATCTTTG	2938	ACAACAGATGAAAGAGTCACTCTGATGCGCATCAACAGGAGTAATTAATCTTTG	2938
Oy	544	AlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProGlnLeuThr---	562	AlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProGlnLeuThr---	562
Db	2939	CGAGTAACGAATGTACCGCAGGAATATTCCGTGATGAAGAG-----TATTGACAGGA	2999	CGAGTAACGAATGTACCGCAGGAATATTCCGTGATGAAGAG-----TATTGACAGGA	2999
Oy	563	-----AspLeuAspPhePheIlePro-----	569	-----AspLeuAspPhePheIlePro-----	569
Db	2993	AAAGCATTAAGCTGTGTCAGAGAGACAAACCACTAAATAATTCATTAAAGAAAACATT	3052	AAAGCATTAAGCTGTGTCAGAGAGACAAACCACTAAATAATTCATTAAAGAAAACATT	3052
Oy	570	AsnAsnAsnLysTyrGln-----SerLeuIleGlyThrGlnThrHisPro	584	AsnAsnAsnLysTyrGln-----SerLeuIleGlyThrGlnThrHisPro	584
Db	3053	GATACACACTGTTTACACAGTCAAGATTCAACGATTATGTCGGCGATTCTAGGAAACCA	3112	GATACACACTGTTTACACAGTCAAGATTCAACGATTATGTCGGCGATTCTAGGAAACCA	3112
Oy	585	GluAspLeuValAspIleIleArgMetGluAspLysLys---GluValIleProValThr	603	GluAspLeuValAspIleIleArgMetGluAspLysLys---GluValIleProValThr	603
Db	3113	GAAGAG-----AAGTTTGTTTCAGCAACAGATTAACAGCAAGCTGACAGCTCCCTCGAA	3166	GAAGAG-----AAGTTTGTTTCAGCAACAGATTAACAGCAAGCTGACAGCTCCCTCGAA	3166
Oy	604	HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPhe	623	HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPhe	623
Db	3167	-----AAATACAGTGTTCAGGTCAAGTTGATTAACANCAAAAGCAGGCTT	3211	-----AAATACAGTGTTCAGGTCAAGTTGATTAACANCAAAAGCAGGCTT	3211
Oy	624	HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr	643	HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr	643

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Db      3212  TATCCAAATATTATTCACGAGCAGCAAGGTAAACAACAAACAGCCGTATGACCGCTCAAAACC 3271
QY      644    AsplysthranLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663
Db      3272  GACCAATCTAGTATGAGGTCAAGAT-----ACAACGATTTATGTT-----GGCAT 3319
QY      664    SerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSer 683
Db      3320  TCGTGCGA-----CCAGAA-----GATTAATTTTCGTTACGCGACACACAA 3361
QY      684    GluGlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700
Db      3362  ACAGGTCAAGACGTCGTCGTTGAAATAATGATGTTCAAGGCAACAGGAAT-----GTT 3415
QY      701    SerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsn 715
Db      3416  GATTAATAATAGC-----GATTAATGCAATGCTATATAATAAAT 3451

RESULT 12
ABN98186
ID      ABN98186 standard; DNA: 4249 BP.
AC      ABN98186;
XX      05-AUG-2002 (first entry)
XX      E faecalis EF104 gene fragment.
XX      Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic;
XX      gene; ds.
XX      Enterococcus faecalis.
XX      US2002045737-A1.
XX      18-APR-2002.
XX      04-MAY-1998; 98US-0071035.
XX      04-MAY-1998; 98US-0071035.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Chol GH, Bailey C, Hromocky] A, Kunsch CA;
XX      MPI: 2002-425450/45.
XX      P-PSDB; ABP43430.
XX      New genes and polypeptides from Enterococcus faecalis, useful as
XX      PT vaccines for preventing, treating or attenuating an infection caused by
XX      PT a member of the Enterococcus genus in an animal, particularly E.
XX      PT faecalis -
XX      Claim 1; Page 183-185; 255pp; English.
XX      The present invention provides the protein and coding sequences of a
XX      CC number of polypeptides from Enterococcus faecalis. The proteins can be
XX      CC used as vaccines for preventing or attenuating an infection caused by a
XX      CC member of the Enterococcus genus in an animal, particularly E. faecalis.
XX      CC The polynucleotide is also useful for preventing or treating E. faecalis
XX      CC infection. The present sequence is a coding sequence of the invention.
XX      SQ      Sequence 4249 BP; 1579 A; 779 C; 815 G; 1069 T; 7 other;

Alignment Scores:
Pred. No.: 0.00911 Length: 4249
Score: 161.00 Matches: 159
Percent Similarity: 34.83% Conservative: 104
Best Local Similarity: 21.06% Mismatches: 326
Query Match: 4.08% Indels: 166
DB: 24 Gaps: 40

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QY 39 AlaleuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56
Db 1451 TCATTAACTACCTGTTAAATGGTCTTAATAAAGCCATTCAATTATCCGATCAATAT 1510
QY 57 ---SerThrProAsnAlaIleAsnProAspSerSerGluTyrArgTyrPylGlyTyr 75
Db 1511 ATTGAACCAATTAGTGTGTTAAATCCT---TTGAATGCTGAAGACGCTGGGATTAATAT 1567
QY 76 GluSerTyrValArgGlyHisProTyrTyrLysGluPheArgValAlaHisAspLeuArg 95
Db 1568 GATCAAA-----AATGGTGGCTATTCATCAAGA 1594
QY 96 -----ValAsnLeuGluGlySerArgSerTyrGluValTyrCysPheAsnLeuLysLys 113
Db 1595 ACACTGCTCTCGATTATGGAGAGCAAGAAACCGATTCAAAATTTAGAAATTTAAAGTA 1654
QY 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrPylLysLys 129
Db 1655 AAGCATCCTTAATTATCTTTCATTACGAGCTACAAAGAAATTTATTTATTTATACAG--- 1711
QY 130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149
Db 1712 -----TTAGGAACG-----GATTATACAGTAACGCCCAACGTCAGATGTTCA 1753
QY 150 GluLeuAsnGluLysLeuArgAlaValMetTyrAsnGlyHisProGluAsnAlaLysnGly 169
Db 1754 GTTATTAACTCAGTACGCCCAATTAACCAACCAATTCAAATTCGATTGTTTAAATAT 1813
QY 170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
Db 1814 GTGCCAGATAGTATGCCAAAGATAAAGATAGTAAAGTACGATACATCCGATTAACATG 1873
QY 185 GluAlaValIlePylTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
Db 1874 AGTGGTGAAGTTTAACCTCAGTTGATACGAGAGTACTACT-----AATGATAG 1924
QY 205 ArgGluSerGluSerAsnLeuValSerThrSerGluLeuSerLeuMetArgGluAlaLeu 224
Db 1925 CGTGGTCTGAACGACACTTCANAGTAAAGTAAATCAATTCCTGTCATACGCAAGAAAT 1984
QY 225 LysGluLeuIleAspProAsnLeuAlaThrLysMetProLysGluValProAspAspHe 244
Db 1985 GATCTTTTGACTACCTAAGCGTCCGTACAAAAATTTCCAGCTGGCGCC-----GATGT 2038
QY 245 GluLeuSerIlePheGluSerGluAspLysGlyTyrAsnLysGlyTyrGlnAsn 264
Db 2039 CTTTGTGACATTTAATGATGTTTCAAAAC-----GATCAGATGATTCATTAATATCCACA 2092
QY 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProMetPro 284
Db 2093 TACTGGAGACCGCGCATACTTCTTAATAACCAATGAGCCCAACAGCCCTGGATATCCA 2152
QY 285 -----ProAsnGluProGluThrThrSerValLeuIle-----Arg 296
Db 2153 ACGATTACTTTTGAAGAAATATAGTATACAGTGTGATTGGAATAAACCAACAA 2212
QY 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGluGlyAlaThrLeuGln 313
Db 2213 CGTTACATTATTT---GAGTATAAAAACGCCAATGGCTGATCGAGTGCACCACTTTAT 2269
QY 314 LeuThrGly-----AspAsnValAsnSerPheGluAlaArgValPhe 327
Db 2270 ATAACAGGACAGCAAGAAACCAACATCGAATATATGAAGCTGCTGCTTCT 2329
QY 328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347
Db 2330 GTTCAAAAT-----GAAGCGTTAGACATTGAGTGCACAA----- 2365
QY 348 LeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGly 367
Db 2366 -----CAAGCGGCGAATCCACATTAATAAAAGTAAACAAAG 2404
QY 368 LysValTyrThr-----IleLeuAspGlyLys-----GluIleGluAsnProAsnLysGlu 384
Db 2405 ACAGTAAACACAAAAATATATGATTAATAACACATCGGTGTAATAATCCACGTTGAA 2464
QY 385 IleValGluProTyrSerValGluValIleTyrAsnAspPheGluGluPheSerValLeuThr 404
Db 2465 TTAACACCAAAAGGACAAACCAATGCTCAATATCGAATTTGAATTCATTACGCTG----- 2518
QY 405 ThrGluAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGluValVal 424
Db 2519 -----AAAGCGGTGCGCAAGATGCT 2539
QY 425 TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
Db 2540 TAT-----TCATTAGAAAGACTCAACAGGTGCGCAAGTCAAT 2578
QY 445 ThrProAspPheThrThrGlyGlu-----ValLysTyrThrHisIleAlaGlyArg 461
Db 2579 TTTAAAGACTATACATTCGACAGAAACATTTAGATTAATACATACAGGCTCTGCAAC 2638
QY 462 AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481
Db 2639 GCTGGCCAAATCTATACAGAAACAAACAAATCGACTGTGAACATTCGAACCGATGCTGCT 2698
QY 482 IleLysLysValIle-----GluLys 488
Db 2699 AGCAAGAAAAAGTCAACACCTCGCCCAATCACATTGAATTCGAAAGGTATCGGAA 2758
QY 489 GlyTyrArgGluLysGlyAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArg 508
Db 2759 GGTATTGTTTATTTAGCAACTGCGACATTCATACGCAATACGTAGAGATGAACAA 2818
QY 509 AlaIleThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerIleGluLeu 524
Db 2819 GCATATGGCAAGGTTCTTTTGAACATAATGTAGATGCGACATACAGCAACCAATTT 2878
QY 525 AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet---AsnAspSerThrLeu 543
Db 2879 ACAACAGATGAAAAAGGTCAATACCTCTTGATGCGCATCAATGACAGGTGATATATCTTG 2938
QY 544 AlaValAlaLysIleLeuValGluTyrAlaGluAspSerAsnProGluLeuThr--- 562
Db 2939 CGAGTAACGAATGTACCGGAGGAATATTCGCGATGAAGAG-----TATTGACAGGA 2992
QY 563 -----AspLeuAspPheIlePro----- 569
Db 2993 AAAGCATTAACTGCTCAAGAGACAAACCACTAAATTAATTCATTAAACGAAACAAAT 3052
QY 570 AsnAsnAsnLysTyrGln-----SerLeuIleGlyThrGlnThrPheAsp 584
Db 3053 GATCAGAGTCTGTTTCAAGTCAAAATTCACGATTTATGTGCGGATTCATGAAACCA 3112
QY 585 GluAspLeuValAspIleIleArgMetGluAspLysLys---GluValIleProValThr 603
Db 3113 GAAGAG-----AAGTTGTTTCCACCAACAGATTAACAGGTCAAGAGTCCCTTCGAA 3166
QY 604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspHe 623
Db 3167 -----AAATTCCTGTTTCCAGGTCAAGTTGATTAACNCAACAGCGCTT 3211
QY 624 HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr 643
Db 3212 TATCCAAATTAATTACAGTACAGCAAGTAAAGAAAGAACAGCTATGTGACCTCAAAACC 3271
QY 644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663
Db 3272 GACCAATCATAGTTAGAGTCAAAAGAT-----ACAACGATTTATGTT-----GGTAT 3319
QY 664 SerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSer 683
Db 3320 TCGTGGA---CCAGAA-----GATAATTCGTTGACGCGCAACAGAA 3361
QY 684 GluGlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700

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Db      3362 ACAGGTCAAGACGCGTTGTAAGAAATTCATGCTTCAGGAACAGTGAAT-----GTT 3415
QY      701 SerLysThrGlyIleThrSerAspGluThrLeuAlaIleGluAsn 715
Db      3416 GATTAATAATAGGC-----GATTATGAATAATGCTATATAAAT 3451
.RESULT 13
ABX61756
ID      ABX61756 standard; DNA: 4249 BP.
AC      ABX61756;
XX
DT      26-FEB-2003 (first entry)
XX
DE      Enterococcus faecalis EF040 polynucleotide #202.
XX
KW      EF040; gene; ds; immunostimulant; antibacterial; gene mapping.
XX
OS      Enterococcus faecalis.
XX
PN      US6448043-B1.
XX
PD      10-SEP-2002.
XX
PF      04-MAY-1998; 980S-0071035.
XX
PR      06-MAY-1997; 97US-044031P.
PR      16-MAY-1997; 97US-046655P.
PR      14-NOV-1997; 97US-066099P.
PR      14-NOV-1997; 97US-066099P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Choi GH, Bailey C, Hromockyj A, Kunsch CA;
XX
DR      WPI; 2003-089120/08.
DR      P-PSDB; ABU13709.
XX
PT      New EF040 polypeptides and polynucleotides from Enterococcus faecalis,
PT      useful for generating an immune response against E. faecalis and other
PT      Enterococcus species, and as vaccines against other bacterial genera -
XX
XX      Example 1; Column 205-208; 146bp; English.
XX
XX      The invention relates to polynucleotide fragments of a gene from
XX      Enterococcus faecalis, EF040, and the polypeptides encoded by them. The
XX      polypeptides are useful in detecting E. faecalis, as epitope tags, as
XX      molecular weight markers on SDS-PAGE gels or for molecular sieve gel
XX      filtration columns, in generating antibodies that specifically bind to
XX      the E. faecalis polypeptides, in generating an immune response against E.
XX      faecalis and other Enterococcus species and as vaccines against other
XX      bacterial genera. The polynucleotides are useful as probes for gene
XX      mapping and for identifying E. faecalis in biological samples. Sequences
XX      CC AAX61555-ABX61802 represent EF040 polynucleotides of the invention.
XX      CC Note: The sequence data for this patent can also be obtained from USPTO
XX      at seqdata.uspto.gov/sequence.html.
XX
SQ      Sequence 4249 BP; 1579 A; 779 C; 815 G; 1069 T; 7 other:

Alignment Scores:
Pred. No.: 0.00911 Length: 4249
Score: 161.00 Matches: 159
Percent Similarity: 34.83% Conservative: 104
Best Local Similarity: 21.06% Mismatches: 326
Query Match: 4.08% Indels: 166
DB: 25 Gaps: 40

US-09-494-297-2 (1-757) x ABX61756 (1-4249)
QY      39 AlaleuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56
Db      1451 TCATTAAAGTACACCTGTAATTTGGTCTCAATTAAGCCATTGCATTAATGATTCGATCAATAT 1510

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QY      57 ----SerThrProAsnAlaIleAsnProAspSerSerGluTyrArgTyrGlyTyr 75
Db      1511 ATTGAACCAATTAAGTGTGTTAATCCCT---TTGATCTGTAACTGCTGGGTAATAT 1567
QY      76 GluSerThrValArgGlyHisProTyrTyrGlnPheArgValAlaHisAspLeuArg 95
Db      1568 GATCAA-----AATGGTGCCTATTCATCAAGA 1594
QY      96 ----ValAsnLeuGlySerArgSerTyrGlnValTyrGlyPheAsnLeuLysLys 113
Db      1595 ACAACTGCTTCAGTTATGGAGAGCAAGCAAAACCGATTCATAAATTAGAAATTAAGAATA 1654
QY      114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrTyrLysLys 129
Db      1655 AAGCATCTTAATTAATCTTTCATTCAGAGCTACCAAAAGAAATTAATTTTATTCACAG--- 1711
QY      130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149
Db      1712 ----TTAGGAACG-----GATTATACAGTAAACGCAACGTCAGATGTTCA 1753
QY      150 GluLeuAsnGlnLysLeuArgAlaValaMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169
Db      1754 GTTATTAAAGTTCACCTACGCCAATTAACCAAGCAAAATCCAAATTCGTTTAAATAT 1813
QY      170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
Db      1814 GTGCCAGATAGTGTGGCAAAAGATAAAGATATCCAGTCCATACGATACCGATACCAATG 1873
QY      185 GluAlaValIlePyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
Db      1874 AGTCTGAAGGTTAACTCCAGTTACGACAGCACTACT-----AATAGTAAG 1924
QY      205 ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
Db      1925 CGTGGTTCTGAAGCAACACTTCAAGTAGTAATAATCAATTCCTTGCAATGCAAGCAAT 1984
QY      225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
Db      1985 GATTCCTTTGACACACACGACGTCGTCGCAAAATTCACCTGACGCGCC-----GATGTT 2038
QY      245 GluLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264
Db      2039 CTTTGTGACATTTATGATGTTTCAAC-----GATCAGGTATGATCAATTTTCCACAA 2092
QY      265 LeuLeuSerGlyLeuValProThrLysProThrProGlyAspProPheMetPro 284
Db      2093 TACTGGACCGCGGTCAATCTTGTGATTAACCAATGACGCCAAACACCCCTGATATCCA 2152
QY      285 ----ProAsnGlnProGlnIleThrThrSerValLeuIle-----Arg 296
Db      2153 ACGATTACTTTTACGCAAAATACCAATAGTTACAGCTTATTTGGAAACCAACAA 2212
QY      297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGluGlyAlaThrLeuGln 313
Db      2213 CGTTACATTTATTT---GAGTATTAATAACGCCAATGCTGTGACAGCGCCAACTTTTAT 2269
QY      314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327
Db      2270 ATTAACAGGACACAGCAAGCAACCAATGCAATTAATTAATGAAGCTGTGCTTGCTTCT 2329
QY      328 SerSerAsnAspIleGlyIleGluArgIleGluLeuSerAspGlyThrThrLeuThrGlu 347
Db      2330 GTTCAAAAT-----GAAGGCTTAAGACATTTTGATGTCACAA----- 2365
QY      348 LeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGly 367
Db      2366 ----CAAGCGCGCAATTCACCAATTAATAAATGTAACCAAAACG 2404
QY      368 LysValTyrThr---IleIleAspGlyLys-----GlnIleGluAsnProAsnLysGlu 384
Db      2405 ACAGTAAACAACAAAAAATATTGATTAATTAATAACATCGTGTGAATAATCCACGATTGAA 2464

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QY 385 ILeValGluProTyrSerValGluIalTyrAsnAspPheGluGluPheSerValLeuThr 404
Db 2465 TTAACACCAAAAGGCACAAACCAATCGTCAATGATTGGAATTCATTACCGTG----- 2518
QY 405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal 424
Db 2519 -----AAAGCGTGCCGACAAACATGCT 2539
QY 425 TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
Db 2540 TAT-----TCATTAGAGAAAGACTACAAAGCGTGCCGAAAGTCAT 2578
QY 445 ThrProAspPheThrThrGlyGlu-----ValLysTyrThrHisIleAlaGlyArg 461
Db 2579 TTTAAAGACTATCTATACAGAAACATTCAGATGATGAATACAGGTCTCTCCAAAC 2638
QY 462 AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481
Db 2639 GCTGGCCAAATCTATACAGAAACACAAATCGACTGTGAACATGACCAAGTATGCTGCT 2698
QY 482 IleLysLysValIle-----GluLys 488
Db 2699 AGCAAGAAAGAAAGTACACATCGCCCAATCACATTGAATTCAGAAAGTGATCGCGAA 2758
QY 489 GlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArg 508
Db 2759 GGTATTTGTTTATTATGCAACATGCCACATTCTACAGCATACGTTAGAGATGAAACCA 2818
QY 509 AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerAlaGluLeu 524
Db 2819 GCAATTTGGGAAGGTTCTTTGCACTAATGATATGTCACCAATACAGCAACGCAATTT 2878
QY 525 AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet---AsnAspSerThrLeu 543
Db 2879 ACAACAGATGAAAGAGTCAATATCTCTTGATGCCATGACACAGTGATATATCTTTG 2938
QY 544 AlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProGlnLeuThr--- 562
Db 2939 CGAGTACGAATGTACCGCAGGAATATTCCTGGATGAGAG------TATTGACAGGA 2992
QY 563 -----AspLeuAspPhePheIlePro----- 569
Db 2993 AAAGCCATTAAAGCTGTCAAGAGACAAACCACTAAATAATTCATTAAACGAAACAAAT 3052
QY 570 AsnAsnAsnLysTyrGln-----SerLeuIleGlyThrGlnThrHisPro 584
Db 3053 GATCAGCTGCTTTACAGTCAAGTCAAGATTCACAGATTTATGTCGGCATTCATCAAGAACCA 3112
QY 585 GluAspLeuValAspIleIleArgMetGluAspLysLys---GluValIleProValThr 603
Db 3113 GAAAG-----AACTTTGTTTCAGCAACAGATTAACAGATTCAGACGTTCCCTTCGAA 3166
QY 604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspHe 623
Db 3167 -----AAATCAGCTGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3211
QY 624 HisPheGluIleGluLeuLysAsnLysGlnGluLeuLeuSerGlnThrValLysThr 643
Db 3212 TATCCAAATTAATTAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3271
QY 644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663
Db 3272 GACCAATCATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3319
QY 664 SerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGluThrAspSer 683
Db 3320 TCGTGGAAA-----CCAGAA-----GATTAATTCGTTTCACCGCAGCAACAA 3361
QY 684 GluGlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700
Db 3362 ACAGGTCAAGACGTTCCGTTTGAAATAATTTGATGTTCAAGGCAACGTAAT-----GTT 3415
QY 701 SerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsn 715

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Db 3416 GATAAAATATGCG-----GATTATGAAATGTTCTATATAAAT 3451
RESULT 14
ID AAX20200
AAX20200 standard; DNA; 4359 BP.
XX
AC AAX20200;
XX
DT 20-APR-1999 (first entry)
XX
DE Enterococcus faecalis gene EF104.
XX
KW Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
XX detection; attenuation; antigenic; ss.
XX
OS Enterococcus faecalis.
XX
PN M09850554-A2.
XX
PD 12-NOV-1998.
XX
PF 04-MAY-1998; 98WO-US08959.
XX
PR 14-NOV-1997; 97US-0066009.
PR 06-MAY-1997; 97US-0044031.
PR 16-MAY-1997; 97US-0046653.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bailey C, Chol GH, Hromocky J A, Kunsch CA.
XX
DR WPI: 1999-070095/06.
XX P-PSDB: AAY0210.
XX
PT New isolated Enterococcus faecalis polynucleotides - used to develop
PT products for the detection of Enterococcus and for use in vaccines
PT for prevention or attenuation of Enterococcus infection
XX
PS Claim 1; Page 200-201; 301pp; English.
XX
CC The present sequence represents a gene isolated from
CC Enterococcus faecalis. The present invention describes genes, proteins
CC and antigenic polypeptides isolated from E. faecalis. The proteins can
CC be used in vaccines for preventing or attenuating an infection caused
CC by a member of the Enterococcus genus in an animal. They can also be
CC used for detecting Enterococcus antibodies in a sample. The nucleotide
CC sequences can be used for detecting Enterococcus nucleic acids.
CC products from the present invention can also be used for screening
CC compounds to identify agonists and antagonists of E. faecalis protein
CC activity.
XX
SQ Sequence 4359 BP; 1614 A; 794 C; 838 G; 1106 T; 7 other;
XX
Alignment Scores:
Pred. No.: 0.0094 Length: 4359
Score: 161.00 Matches: 159
Percent Similarity: 34.83% Conservative: 104
Best Local Similarity: 21.06% Mismatches: 326
Query Match: 4.08% Indels: 166
DB: 20 Gaps: 40
US-09-494-297-2 (1-757) x AAX20200 (1-4359)
QY 39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56
Db 1546 TCATTATAGTACACCGTATATGCTCTATATAAGCCATTCAATTGATCCGATCAATAT 1605
QY 57 ---SerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTyrTyrGlyTyr 75
Db 1606 ATTGAACCAATATAGTGTGTTAATCCT---TTGAAATGCGAAGAACTGGGCTAATATAT 1662
QY 76 GluSerTyrValArgGlyHisProTyrTyrTyrLysGlnPheArgValAlaHisAspLeuArg 95

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Db 1663 GATCAA-----ATGTCCTTATTCATCAGA 1689
 Qy 96 -----ValasnleugllyserArgSerTyrGlnValTyrCysPheAsnLeuLys 113
 Db 1690 ACAACTGTCTCATGTTATGAGCAAGAACCCGATTCAAAATTTAGAAATTAAGTA 1749
 Qy 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrPheLys 129
 Db 1750 AAGATCCTTAATATCTTCATTATCGAGCTACAAAACAATTTTATTTATTCACAG--- 1806
 Qy 130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149
 Db 1807 -----TTAGACAG-----GATTATACAGTACGCCACGTCAGATGGTTCA 1848
 Qy 150 GluLeuasnGlnLysLeuArgAlaValMetTyrAsnGlnLysProGlnAsnAlaAsnGly 169
 Db 1849 GTTATTTAGTTCACTACGCCAATTAACCAAGAAATCCAAATTCCAATGGTTTAAATAT 1908
 Qy 170 IleMetGluLysLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
 Db 1909 GTGCACAGATAGTTTGGCAAAAAGATAAAGTATCCAGTCGATACGATACGATACAAATG 1968
 Qy 185 GluAlaValTrrPyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
 Db 1969 AGTGCCTGAAGGTTTAACTCCAGTTGATACGACAGTACTACT-----AATAGTAG 2019
 Qy 205 ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
 Db 2020 CGTGCTCTGACACCAACACTTCAAAAGTAGTAAATAATTCCTTGTCATGCACGAAT 2079
 Qy 225 LysGlnLeuLysProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
 Db 2080 GATTCTTTTACTACACTACGATCCGACAAAATTCACAGTCCAGTCCGCGC-----GATGTT 2133
 Qy 245 GlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264
 Db 2134 CTTTTCGACATTTATGATGTTTCAAC-----GATCAGTAGATTCATTAATTTATCCAA 2187
 Qy 265 LeuLeuSerGlyLysLeuValProThrLysProProThrProGlyAspProPhePro 284
 Db 2188 TACTGGAGCGCGCTCATACTTTGATTAACCAATGACGCCAAACACCCCTGGATGCCA 2247
 Qy 285 -----ProAsnGlnProGlnThrThrSerValLeuLe-----Arg 296
 Db 2248 ACGATTACTTTTACGAAATACCAATATGATTACGTTGATTTTGAAACCAACAA 2307
 Qy 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGluGlyAlaThrLeuGln 313
 Db 2308 CGTTACTTATTT--GAGTATAAAAACGCCAATGCTGATCGACGTCGAACCTTTAT 2364
 Qy 314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327
 Db 2365 ATTAACAGGACAGCAAGAAAGAACCAATCGAATATATATGAGGCTCTGCTGGTTCT 2424
 Qy 328 SerSerAsnAspIleGlyLysArgIleGluLeuSerAspGlyTyrThrLeuThrGlu 347
 Db 2425 GTTCAAAAT-----GAAGCGTTAGACATTTTGATGCCAACAA----- 2460
 Qy 348 LeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGly 367
 Db 2461 -----CAAGCGCGCAATCCAAATTAATAAATGTAACAAAACG 2499
 Qy 368 LysValTyrThr-----IleIleAspGlyLys-----GlnIleGluAsnProAsnLysGlu 384
 Db 2500 ACAGTACACACAAAAATATGATTAATAAACAACATCGTGTGAAAAATCCACAGATTGAA 2559
 Qy 385 IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThr 404
 Db 2560 TTAAACACCAAAAGCAACCAACCAATGCTCAATCGATTGAATCTATACCGG----- 2613
 Qy 405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal 424

Db 2614 -----AAAGCGTCCAGAGATGCT 2634
 Qy 425 TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
 Db 2635 TAT-----TCATTAGACAGACTCAACAAAGGTGGGAAGTCAAT 2673
 Qy 445 ThrProAspPheThrThrGlu-----ValLysTyrThrHisIleAlaGlyArg 461
 Db 2674 TTTAAACATATACATTATGACAGAAAACATTACGATGGAATATACATACGCTCGCAAC 2733
 Qy 462 AspleuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481
 Db 2734 GCTGGCCAAATCTATACAGAAACAACAAATGACCTGTGAACATTTGAACAGATGCTGCT 2793
 Qy 482 IleLysValIle-----GluLys 488
 Db 2794 AGCAGAAAAGTCCACCACTGCCCAATCATTCATTAATTTCCAGAAAGTATGCCGAA 2853
 Qy 489 GlyTyrArgGluLysGlnAlaIleGluTyrSerGlyLeuThrGlnThrGlnLeuArg 508
 Db 2854 CGTATGTTTATTTAGCAACTGCCACATCTACACGCAATACGTAGAGATGAAACCAA 2913
 Qy 509 AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerAlaGluLeu 524
 Db 2914 GCATTTCCGAAGGTTCTTTGAACTAATGATATGTCACGATACGACGACCGAATTT 2973
 Qy 525 AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet--AsnAspSerThrLeu 543
 Db 2974 ACAACATGACAAAAGTCAATCTCTTGATGCCATCATGACAGAGTGTATATCTTTC 3033
 Qy 544 AlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGlnLeuThr-- 562
 Db 3034 CGAGTACGATGACGACGACGAGATATTCGCTGATGAAAG-----TATTGACACGA 3087
 Qy 563 -----AspleuAspPheThrLeuPro----- 569
 Db 3088 AAAGCATTAAGCTGTCAAGAGACACCAACCACTAAATATTCATTAAACGAAACAAAT 3147
 Qy 570 AsnAsnAsnLysTyrGln-----SerLeuIleGlyThrGlnTrrPheLysPro 584
 Db 3148 GATCACAGTGTGTACAGCAAGTCAACGATTAATATCGCGCATTAATGGAACCA 3207
 Qy 585 GluAspLeuValAspIleIleArgMetGluAspLysLys--GluValIleProValThr 603
 Db 3208 GAAGAG-----AACTTTGTTTCAACAGCAAGATTAACAGGTCAAGACGTTCCCTTCAA 3261
 Qy 604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPhe 623
 Db 3262 -----AAATTCAGTGTTCAGGTCAAGTGTATGATACANCAAGACGCGTT 3306
 Qy 624 HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr 643
 Db 3307 TATCCATTTTATTAACATGACGAAAGTAAAGAAAGAACACCCATATGACCGTCAAAACC 3366
 Qy 644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663
 Db 3367 GACCAATCTAAGTTAGAGGTCAAAAGAT-----ACAACGATTTATGTT-----GGTGA 3414
 Qy 664 SerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSer 683
 Db 3415 TCGTGCAAA-----CCAGAA-----GATTAATTCGTTTCAGCGACGACGACAA 3456
 Qy 684 GluGlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700
 Db 3457 ACAGGTCAACACGTCGCTTTGAAAAAATGATGATTCACGAGAACAGTGAAT-----GTT 3510
 Qy 701 SerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsn 715
 Db 3511 GATTAATAATAGC-----GATTATGAATATGTCTATAAAT 3546
 RESULT 15
 ABBN8185
 ID ABBN8185 standard; DNA: 4359 BP.

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XX ABN98185;
AC
XX
XX 05-AUG-2002 (first entry)
DT
XX
XX E faecalis EPI04 gene.
DE
XX
XX Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic;
KM gene; ds.
XX
XX Enterococcus faecalis.
OS
XX US2002045737-A1.
XX
XX 18-APR-2002.
PD
XX
XX 04-MAY-1998; 98US-0071035.
PF
XX
XX 04-MAY-1998; 98US-0071035.
PR
XX
XX (HUMA-) HUMAN GENOME SCL INC.
RA
XX
XX Choi GH, Bailey C, Hromockyj A, Kunsch CA;
PI
XX
XX MPI; 2002-425450/45.
DR
XX
XX P-PSDB: ABP43429.
XX
XX New genes and polypeptides from Enterococcus faecalis, useful as
PT vaccines for preventing, treating or attenuating an infection caused by
PR a member of the Enterococcus genus in an animal, particularly E.
PT faecalis.
XX
XX
XX Claim 1: Page 180-182; 255pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of a
CC number of polypeptides from Enterococcus faecalis. The proteins can be
CC used as vaccines for preventing or attenuating an infection caused by a
CC member of the Enterococcus genus in an animal, particularly E. faecalis.
CC The polynucleotide is also useful for preventing or treating E. faecalis
CC infection. The present sequence is a coding sequence of the invention.
CC
XX
XX
XX Sequence 4359 BP; 1614 A; 794 C; 838 G; 1106 T; 7 other;
SQ

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Alignment Scores:

Pred. No.:	Length:	4359
Score:	0.0094	159
Percent Similarity:	161.00	104
Best Local Similarity:	34.83%	326
Query Match:	4.08%	166
DB:	24	40

US-09-494-297-2 (1-757) x ABN98185 (1-4359)

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OY 39 AlaleuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGlySer----- 56
   ||||| ||| ||||| ||| ||||| |||||
DB 1546 TCATTAACTACACCTGTAATGGTCTAATAAGCATTCATTAGTATCCGATCAATAT 1605
   ||||| ||||| ||||| ||||| ||||| |||||
OY 57 ---SerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTyrGlyTyr 75
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1606 ATTGAAACCAATTAAGTGTGTAATCCT---TTGAATGCTGAAACGTCGTGGGTAATAT 1662
   ||||| ||||| ||||| ||||| ||||| |||||
OY 76 GluSerTyrValArgGlyHisProTyrTyrLysGlnPheArgValAlaHisAspLeuArg 95
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1663 GATCA-----AATGCTGCTATTCATCAAGA 1689
   ||||| ||||| ||||| ||||| ||||| |||||
OY 96 -----ValAsnLeuGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1690 ACAACTGCTCAGTTATGGGAAGCAAGAAACGATTCAAATTTGAATATTAAGTA 1749
   ||||| ||||| ||||| ||||| ||||| |||||
OY 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrTyrLysLys 129
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1750 AAGCATCTCAATTATCTTTCATTACGACCTACAAAGAAATTTATTTTATACAAAG--- 1806
   ||||| ||||| ||||| ||||| ||||| |||||

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OY 130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1807 -----TTAGGAACG-----GATTATACAGTACGCACTGACATGCTTCA 1848
   ||||| ||||| ||||| ||||| ||||| |||||
OY 150 GluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1849 GTTATTAACTCAGTACAGCAATTAACCAAGAAATCCAAATTTGTTTAATATAT 1908
   ||||| ||||| ||||| ||||| ||||| |||||
OY 170 IleMetGlyGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1909 GTGCCAGTAGTTTCCAAAGATTAAGTATACCGATCCGATACCATCCGTAACAATG 1968
   ||||| ||||| ||||| ||||| ||||| |||||
OY 185 GluAlaValTyrPtyTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1969 AGTGCTGAAGTTTACTTCCAGTTCATACGACGATCACTACT-----AATGCTAAG 2019
   ||||| ||||| ||||| ||||| ||||| |||||
OY 205 ArgGluSerIlePheGluSerGlnValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2020 CGTGCTTCGAAAGCAACACTTCAAAGTAAATCAATTCCTTGTCATACAGCAAT 2079
   ||||| ||||| ||||| ||||| ||||| |||||
OY 225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2080 GATTCCTTTGACTCCTACGAGCGTCCGTCACAAATTCACAGTCGCGCC-----GATGTT 2133
   ||||| ||||| ||||| ||||| ||||| |||||
OY 245 GlnLeuSerIlePheGluSerGlnAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2134 CTTTGTGACATTTAAGATGTTTCAAC-----GATCAGTAGATTCATTTATTCACAA 2187
   ||||| ||||| ||||| ||||| ||||| |||||
OY 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPhePro 284
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2188 TACTCGACCGCGGTCATCTTGTATTAACCAATGACGCCAACGCCCTGATATCA 2247
   ||||| ||||| ||||| ||||| ||||| |||||
OY 285 -----ProAsnGlnProGlnThrThrSerValLeuIle-----Arg 296
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2248 ACGATTACTTTTGACGAAATATACCAATGATTCACGTTGATTTGCAAAACCAACAA 2307
   ||||| ||||| ||||| ||||| ||||| |||||
OY 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGlnGlyAlaThrLeuGln 313
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2308 GATTTCATTATTT---GAGTATTAATAAGCCCAATGCTGATCGACGTCGCCAATCTTTAT 2364
   ||||| ||||| ||||| ||||| ||||| |||||
OY 314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2365 ATACAGGACACGCAAGAACCAACATCGAATATTAATGAAGCTGCTGCTCGTTCT 2424
   ||||| ||||| ||||| ||||| ||||| |||||
OY 328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyTyrThrLeuThrGlu 347
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2425 GTTCAAAAT-----GAAGCGTTAGACATTTGAGCTGCACAA----- 2460
   ||||| ||||| ||||| ||||| ||||| |||||
OY 348 LeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGlnAlaGly 367
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2461 -----CAGCGCGCAATCCACATTTAAATAATGTAAACAAACG 2499
   ||||| ||||| ||||| ||||| ||||| |||||
OY 368 LysValTyrThr---IleIleAspGlyLys-----GlnIleGlnAsnProAsnLysGlu 384
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2500 ACAGTAAACAAACAAATATGATATATAAACAACATCGTGTGAAAAATCCAAACGATTGA 2559
   ||||| ||||| ||||| ||||| ||||| |||||
OY 385 IleValGluProTyrSerValGlnAlaTyrAsnAspPheGluGlnPheSerValLeuThr 404
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2560 TTAAACCCAAAGGACACCAACCAATGCTCAAAATTCGATTGAAATTCATTACCGTG----- 2613
   ||||| ||||| ||||| ||||| ||||| |||||
OY 405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal 424
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2614 -----AAGGCGTCCCAAGAAAGTCT 2634
   ||||| ||||| ||||| ||||| ||||| |||||
OY 425 TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2635 TAT-----TCATTAGGAAGATACCAACAGCGGCGCAAGATCTTT 2673
   ||||| ||||| ||||| ||||| ||||| |||||
OY 445 ThrProAspPheThrThrGlyGlu-----ValLysTyrThrHisIleAlaGlyArg 461
   ||||| ||||| ||||| ||||| ||||| |||||
DB 2674 TTTAAAGCTATACATTGACAAAGAAACATTCAGTATGATCAATACGCTCTGCAAC 2733
   ||||| ||||| ||||| ||||| ||||| |||||
OY 462 AspLeuPheLysTyrThrValLysProArgAspThrAspProThrPheLeuLysHis 481
   ||||| ||||| ||||| ||||| ||||| |||||

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